

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 16, 2005, 21:58:20 ; Search time 11350 Seconds

(without alignments)

4653.408 Million cell updates/sec

Title: US-09-833-222a-10

Perfect score: 5726

Sequence: 1 MAVALGTRRRDRVKLWADTF.....MPMNTVPVLLGGNIRVVAL 1090

Scoring table:

BLOSUM62	Xgapop 10.0 , Xgapext 0.5
Xgapop 10.0 , Xgapext 0.5	
Xgapop 6.0 , Xgapext 7.0	
Deiop 6.0 , Delext 7.0	

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=GenEmbl -OPMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*

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7: gb.ph.*

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11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5399.5	94.3	4604	9 AF516695	AF516695 Homo sapi
2	5386.5	94.1	5073	6 BD248445	BD248445 Alpha-2/d
3	5373.5	93.8	5359	9 HSM805741	BX537437 Homo sapi
4	5342.5	93.3	3339	6 AX098927	AX098927 Sequence

5	5342.5	93.3	3339	6	AX099347	Sequence
6	5276	92.1	3209	6	AX098926	Sequence
7	5276	92.1	3209	6	AX099346	Sequence
8	5244.5	91.6	5001	6	BD248454	Alpha-2/d
9	5239.5	91.5	5960	6	HSM805740	Homo sapi
10	5214.5	91.1	5712	6	BD248455	Alpha-2/d
11	5148	89.9	3201	6	AX098925	Sequence
12	5148	89.9	3201	6	AX099345	Sequence
13	3808	66.5	4125	6	AX302028	Sequence
14	3423.5	59.8	3710	10	MMU010949	AF486278 Rattus no
15	3421.5	59.8	3276	10	AF486278	Homo sapi
16	3421.5	59.8	3544	9	HSJ272268	Homo sapi
17	3416.5	59.7	3276	6	AR454329	Sequence
18	3416.5	59.7	3276	6	AX427033	Sequence
19	3416.5	59.7	3653	9	AF516696	Homo sapi
20	3416.5	59.7	3690	6	AR454328	Sequence
21	3416.5	59.7	3690	6	AX427031	Sequence
22	3410.5	59.6	3770	6	BD248444	Alpha-2/d
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24	3410.5	59.6	3770	6	AX099316	Sequence
25	3400.5	59.4	3213	6	AX098884	Sequence
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27	3326.5	58.1	3114	6	AX098883	Sequence
28	3326.5	58.1	3114	6	AX099303	Sequence
29	3297	57.6	3464	9	HSJ272213	Homo sapi
30	3278.5	57.3	3057	6	AX098882	Sequence
31	3278.5	57.3	3057	6	AX099302	Sequence
32	3222	56.3	3598	6	BD248481	Alpha-2/d
33	2026.5	35.4	2008	6	BD248480	Alpha-2/d
34	1868.5	32.6	2944	9	HSM801956	Homo sapi
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36	1792.5	31.3	1050	6	AX099310	Sequence
37	1695	29.6	969	6	AX098889	Sequence
38	1695	29.6	969	6	AX099309	Sequence
39	1598	27.9	912	6	AX098888	Sequence
40	1598	27.9	912	6	AX099308	Sequence
41	1552	27.1	6395	3	AY069830	Drosophil
42	1497.5	26.2	5862	6	AX155081	Sequence
43	1410	24.6	6519	6	CQ602907	Sequence
44	1362.5	23.8	856	6	AX552194	Sequence
45	1336.5	23.3	3414	6	CQ585735	Sequence

ALIGNMENTS

RESULT 1	AF516695	4604 bp	mrna	linear	PRI 10-SEP-2002
LOCUS	AF516695				
DEFINITION	Homo sapiens voltage-gated calcium channel alpha(2)delta-4 subunit mRNA, complete cds.				
ACCESSION	AF516695				
VERSION	AF516695.1				
KEYWORDS	GI:22770593				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 4604)				
AUTHORS	Qin,N., Yagel,S., Momplaisir,M.L., Codd,E.E. and D'Andrea,M.R.				
TITLE	Molecular Cloning and Characterization of the Human Voltage-Gated Calcium Channel alpha(2)delta-4 Subunit				
JOURNAL	Mol. Pharmacol. 62 (3), 485-496 (2002)				
MEDLINE	22169250				
PUBMED	12181424				
REFERENCE	2 (bases 1 to 4604)				
AUTHORS	Qin,N., Yagel,S., Momplaisir,M.L., Codd,E.E. and D'Andrea,M.R.				
TITLE	Direct Submission				
JOURNAL	Submitted (29-MAY-2002) Drug Discovery, Johnson & Johnson				
FEATURES	Pharmaceutical Research and Development L.L.C., McKean & Welsh Roads, Spring House, PA 19477, USA				
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SDTFFSLGASGHGEYILLGNTSVEEGHLLDHLDALAGDWIYCTIDDDHRLQSLEAMIRFLTRKDPOLECEDELVEFLDAVTPAEAYTWTALALNMESESHVYDMSAFLTRAGLLRSSLFYSGEKVSDRKELTPEDEASVFTLDRFPLMYRQASHEPAGSVFNLFWARGPSAGSPMVVTAATAVAVTDKRTAIAAAGVQMKLEFLQRFKFWAATROCS		Qy		271	TyrValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsn	290
TVDPYVTSQSDLDLCFVIDNNGFILISKRSRETGRFLGKVDGVLTLTOLLNGVFSQVTMYDYQMKCKPSHSHSAQPLVSPISAPLATRATRLQLQLVFLLEWSVWMSGVDRGAEAKSVFHSHKHKQDQPOCDTEPYPVFYPAIREANGIVECGKQCFVVFVQOQIPNSNLLLVDTDPTDCSIFPPVLOEATVKYNASVKDRMRSQKLRRLRPDSCHAFHPHEN		Db		1366	TAGCTCCATTACATCGAGCCTTGTGTTTAAAGGGATCCTCGTCCAGGCGGACCGAGACAAT	1425
AODCGGASDTSAPPLILLPVCAMGLLPQLLR"		Qy		291	ArgGluHisPheLysLeuLeuValGluLeuMetValLysGlyValGlyValValAsp	310
		Db		1426	CGAGACATTTCAACTGCTGTTGGAGGAGTTGATGGTCAAGGTGTGGGGGTCTGGGAC	1485
		Qy		311	GlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySer	330
		Db		1486	CAAGCCCTGAGAGAAGCCCTCCAGATCTCTGAAGCAGTTCCAGAGAGCCCAAGCAAGGAAGC	1545
		Qy		331	LeuCysAsnGlnAlaIleMetIleLeuSerAspGlyAlaValGluAspTyrGluProVal	350
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		Qy		351	PheGluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArg	370
		Db		1606	TTTGAGAGTATTAACCTGGCCAGACTGTAAAGTCCGAGTCTTCTACTTACCTCATTTGGAGA	1665
		Qy		371	GluValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThr	390
		Db		1666	GAAGTGCTTTTGTCTGACCGCATGAAGTGGATTGTCATCAACCAACAAAGGCTACTACAG	1725
		Qy		391	GlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSer	410
		Db		1726	CAGATCTCAACGCTGGCGACACCCAGGAGAACGTTGATGGAATACCTGCACGCTCAGC	1785
		Qy		411	ArgProMetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSer	430
		Db		1786	CGCCCATCGTTCATCAACCCAGCACCATCATCTCGACAGAGCCCTTACATGGACAGC	1845
		Qy		431	LysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProVal	450
		Db		1846	AAAGCTCTCAGCTCGCAGCCTCAGACCTGACACTGCTCACCACCTGTGCCATGCCAGTC	1905
		Qy		451	PheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp	470
		Db		1906	TTCAGCAAGAAACGAAACGCGATCCCATGGCATTTCTCTGGGTGTGGGTGGCTCAGAT	1965
		Qy		471	ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyr	490
		Db		1966	GTGGCCCTGAGAGAGCTGATGAAGCTGGCGCCCCGGGTACAGCTTGGAGTGCACGGATAC	2025
		Qy		491	AlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr	510
		Db		2026	GCCTTTCTGAACACCAACAATGGCTACATCTCTCCATCCCGACCTCCGCGCCCTGTAC	2085
		Qy		511	ArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluVal	530
		Db		2086	AGAGAGGGGAGAAACCTAAACCCCAACCTAACTACACAGTGTGATCTCTCCGAAGTG	2145

ORIGIN

Alignment Scores:									
Pred. No.:	0	Length:	4604						
Score:	5399.50	Matches:	1037						
Percent Similarity:	97.65%	Conservative:	4						
Best Local Similarity:	97.28%	Mismatches:	25						
Query Match:	94.30%	Indels:	1						
DB:	9	Gaps:	0						
US-09-833-222A-10 (1-1090) x AF516695 (1-4604)									
Qy	11	AspArgValLysLeuTrpAlaAspThrPheGlyAspLeuTyrAsnThrValThrLys	30						
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Qy	31	TyrSerGlySerLeuLeuGlnLysLysTyrTyrAspValGluSerSerLeuLysIle	50						
Db	646	TACTCAGGCTCTCTTGTCTGCAGAGAAAGTACAAGGATGTGAGTCCAGTCTGAAGATC	705						
Qy	51	GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu	70						
Db	706	GAGGAGGTGGATGGCTGGAGCTGGTGAAGATCTCAGAGGACATGGAGAACATGCTG	765						
Qy	71	ArgArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsn	90						
Db	766	CGAGAGAAAGTCGAGGCGGTCCAGAACTGGTGAAGTGTCCGAGGAGGCGGACCTGAAC	825						
Qy	91	HisGluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArg	110						
Db	826	CACGAATTCATGAATCCCTGGTGTTCGACTATTACAACTCGGTCTGATCAACGAGAGG	885						
Qy	111	AspGluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHis	130						
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Qy	131	PheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyr	150						
Db	946	TTCAGCAACTTCGGGTGAACACTCCATCAGCAGCGGTGCGGCTGCCACCAACGTTGAC	1005						
Qy	151	AsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPhe	170						

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RESULT 2
BD248445
LOCUS Alpha-2/delta gene.
DEFINITION BD248445
ACCESSION BD248445
VERSION 1 GI:33058215
KEYWORDS JP 2002526100-A/3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 5073)
TITLES Johns, M.A., Moldover, B. and Offord, J.D.
JOURNAL Alpha-2/delta gene
Patent: JP 2002526100-A 3 20-AUG-2002;
WARNER LAMBERT CO
COMMENT OS Homo sapiens (human)
PN JP 2002526100-A/3
PD 20-AUG-2002
PF 07-OCT-1998 JP 2000574561
PR 07-OCT-1998 US 60/103322, 30-OCT-1998 US 60/106473 PR
29-DEC-1998 US 60/114088
PI MARGARET ANN JOHNS, BRIAN MOLDOVER, JAMES DAVID OFFORD PC
C12N15/09, A61K31/711, A61K38/00, A61P25/06, A61P25/08, PC
A61P25/16.
PC A61P25/20, A61P25/22, A61P25/28, A61P25/30, A61P29/00, A61P35/00,
PC C07K14/47,
PC C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12Q1/
02, C12Q1/68,
PC G01N33/15, G01N33/50, C12N15/00, C12N5/00, A61K37/02 CC
Alpha-2/delta gene
FH Key Location/Qualifiers
FT source 1..5073

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Best Local Similarity:	97.09%	Mismatches:	27
Query Match:	94.07%	Indels:	1
DB:	6	Gaps:	0
US-09-833-222A-10 (1-1090) x BD248445 (1-5073)			
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Db	234	TACTCAGGCTCTCTCTTGTCTGCAGAGAGATACAAAGGATGTGGAGTCCAGTCTGAAGATC	293
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REFERENCE 1 (bases 1 to 5359)
AUTHORS Bloecker, H., Boecher, M., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,
Robo, G., Han, M. and Wiemann, S.
TITLE Direct Submission
JOURNAL Submitted (16-JUN-2003) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
This clone (DKFZp686O0495) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/cDNA/.
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Qy 851 ValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMet 870
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Db 3035 TATGACTATCAGGCGCATGTGCAAAACCCCTCGAGTCACCACACAGTCAGCGCCAGCCCTG 3094
Qy 891 ValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnLeuValLeu 910
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Qy 911 PheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSer 930
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Qy 951 TyrProValPheValTyrGlnProAlaIleArgGluAlaAenGlyIleValGluCysGly 970
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RESULT 4
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DEFINITION Sequence 52 from Patent WO0119870.
ACCESSION AX098927
VERSION AX098927.1 GI:13538144
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 Brown, J.P. and Bertelli, P.
AUTHORS Secrated soluble_g(a)2_g(d)-2, g(a)2_g(d)-3 or_g(a)2_g(d)-4
TITLE calcium channel subunit polypeptides and screening assays using
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JOURNAL Patent: WO 0119870-A 52 22-MAR-2001;
FEATURES WARNER-LAMBERT COMPANY (US)
source Location/Qualifiers
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Alignment Scores:
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Best Local Similarity: 97.35% Mismatches: 8
Query Match: 93.30% Indels: 18
DB: 6 Gaps: 2

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Qy 31 TyrSerGlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIle 50
Db 234 TACTCAGGCTCTCTCTGTCTGCAGAGAGAGTACAGGATGTGGAGTCCAGTCTGAAGATC 293
Qy 51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAenMetLeu 70
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Db 414 CACGAATTCATGAATCCCTGGGTTCGCATATTACAACTCGGTCTTCATCAAGAGG 473
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DEFINITION Sequence 52 from Patent WO0120336.
ACCESSION AX099347
VERSION AX099347.1 GI:13538490
KEYWORDS
SOURCE Homo sapiens (human)
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ORGANISM

Homo sapiens

Homo sapiens

Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Bertelli, F., Brown, J. P., Dissanayake, V., Suman-Chauhan, N. and

Gee, N. S.

Screening for alpha2delta-1 subunit binding ligands

Patent: WO 0120336-A 52 22-MAR-2001;

WARNER-LAMBERT COMPANY (US)

Location/Qualifiers

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FEATURES

source

ORIGIN /db_xref="taxon:9606"

Alignment Scores:

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Score: 5342.50 Matches: 1028
Percent Similarity: 97.54% Conservative: 2
Best Local Similarity: 97.35% Mismatches: 8
Query Match: 93.30% Indels: 18
DB: 6 Gaps: 2
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ACCESSION AX098926
VERSION AX098926.1 GI:13538143
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Brown, J.P. and Bertelli, F.
AUTHORS Secreted soluble _g(a)2_g(d)-2, _g(a)2_g(d)-3 or _g(a)2_g(d)-4
TITLE calcium channel subunit polypeptides and screening assays using
same
JOURNAL Patent: WO 0119870-A 51 22-MAR-2001;
WARNER-LAMBERT COMPANY (US)
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ACCESSION AX099346
VERSION AX099346.1 GI:13538489
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1
AUTHORS Bertelli, F., Brown, J.P., Dissanayake, V., Suman-Chauhan, N. and
Gee, N.S.
TITLE Screening for alpha2delta-1 subunit binding ligands
JOURNAL Patent: WO 0120336-A 51 22-MAR-2001;
WARNER-LAMBERT COMPANY (US)
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ACCESSION BD248454
VERSION BD248454.1 GI:33058224
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 5001)
Johns, M.A., Moldover, B. and Offord, J.D.
Alpha-2/delta gene
Patent: JP 2002526100-A 12 20-AUG-2002;
WARNER LAMBERT CO
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PN JP 2002526100-A/12
PD 20-AUG-2002
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REFERENCE 1 (bases 1 to 5960)
AUTHORS Bloeker,H., Boecker,M., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
Robo,G., Han,M. and Wiemann,S.
TITLE Direct Submission
JOURNAL Submitted (16-JUN-2003) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de,
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
This clone (DKF2p686A1395) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at <http://maps.gsfc.de/proj/cDNA/>.
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Db	1437	TTTGAGAAGTATAACTGGCCAGACTGTAAAGTCCGAGTTTTCACTTACCTCATTTGGGAGA	1496
Qy	371	GluValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThr	390
Db	1497	GAAGTGTCCTTTGCTGACCGCATGAAGTGGATTGCATGCAACAAGAGGCTACTACACG	1556
Qy	391	GlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSer	410
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Qy	411	ArgProMetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSer	430
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Qy	431	LysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrValAlaMetProVal	450
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Db	1737	TTCAGCAAGAAGAACGAAACCGATCCCATGGCATTTCTCTGGGTGTGGTGGCTCAGAT	1796
Qy	471	ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyr	490
Db	1797	GTGGCCCTGAGAGAGCTGATGAAGCTGGCGGCCCGGTACAAAGCTTGGAGTGCACGGATAC	1856
Qy	491	AlaPheLeuAnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr	510
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Qy	511	ArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluVal	530
Db	1917	AGAGGGGAGAAACCTAAACCCAACTTAACACAGTGTGGATCTCTCCGAAGTG	1976
Qy	531	GluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr	550
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Qy	571	AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg	590
Db	2097	GACTACTTCTTCACGGACATCAGCGACACCCCTTTTCAGTTTGGGGTGGTGTCTGCCGG	2156
Qy	591	GlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeu	610

Db	2157	GGCCACGGAGAAATACATCTTCTGGGGAAACACGTCTGTGGAAAGAGCCCTGCATGACTTG	2216
Qy	611	LeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspPro	630
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Qy	671	ProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisVal	690
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Qy	771	SerThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAlaAAGlyVal	790
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Qy	791	GlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThr	810
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Qy	811	ValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAsp	830
Db	2817	GTGGATGGGCGGTGCACACAGAGCTGCGAGGACAGTGTATCTGGACTGCTTCGTCTATCGAC	2876
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Qy	871	TyrAspTyrGlnAlaMetCysLysProSerSerHisHisSerAlaAlaGlnProLeu	890
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Qy	891	ValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnLeuValLeu	910
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SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 5712)
TITLE	Johns, M.A., Moldover, B. and Offord, J.D.
JOURNAL	Alpha-2/delta gene
COMMENT	Patent: JP 2002526100-A 13 20-AUG-2002; WARNER LAMBERT CO
OS	Homo sapiens (human)
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PD	20-AUG-2002
PF	07-OCT-1999 JP 2000574561
PR	07-OCT-1998 US 60/103322, 30-OCT-1998 US 60/106473 PR
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DEFINITION Sequence 50 from Patent WO0120336.
ACCESSION AX099345
VERSION AX099345.1 GI:13538488
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Bertelli, F., Brown, J.P., Dissanayake, V., Suman-Chauhan, N. and
Gee, N.S.
TITLE Screening for alpha2delta-1 subunit binding ligands
JOURNAL Patent: WO 0120336-A 50 22-MAR-2001;
WARNER-LAMBERT COMPANY (US)
FEATURES
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ORIGIN
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SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Reddy, R., Thornton, M., Boroweky, M.L., Tang, Y.T., Khan, F.A.,
Tribouley, C.M., Gandhi, A.R., Yao, M.G., Sanjanwala, M.S.,
Baughn, M.R., Nguyen, D.B., Policky, J.L., Yue, H., Seilhamer, J.J.,
Walia, N.K., Lal, P., Kearney, L., Waleh, R.T., Lu, D.A., Greene, B.D.,
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 Klugbauer, N., Lacinova, L., Marais, E., Hobom, M. and Hofmann, F.
 TITLE Molecular diversity of the calcium channel alpha2delta subunit
 JOURNAL J. Neurosci. 19, 648-691 (1999)
 REFERENCE 2 (bases 1 to 3710)
 AUTHORS Klugbauer, N.
 TITLE Direct Submission
 JOURNAL Submitted (10-SEP-1998) Klugbauer N., Institut fuer Pharmakologie

und Toxikologie, Technische Universitaet Muenchen, Biedersteiner Str. 29, 80802, GERMANY
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ORIGIN

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REFERENCE 1 (bases 1 to 3276)
AUTHORS Chu, P.-J. and Best, P.M.
TITLES Molecular cloning of calcium channel alpha(2)delta-subunits from
rat atria and the differential regulation of their expression by
IGF-1
JOURNAL J. Mol. Cell. Cardiol. 35 (2), 207-215 (2003)
MEDLINE 22494975
PUBMED 12606261
REFERENCE 2 (bases 1 to 3276)
AUTHORS Chu, P.-J. and Best, P.M.
TITLES Direct Submission
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Physiology, University of Illinois, 407 S. Goodwin Ave., Urbana, IL
61801, USA
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1024 CTGAACGAGGCTTCAATGACTAGCGGATTTCAACCCACCGGACCAAGGAAGCATTTGC 1083
333 AsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProValPheGlu 352
1084 AGCCAGGCCATATGCTCATACCGACGGCGAGTGGACACCTACGACACCATTTTGCA 1143
353 LysTyrAsnTrpProAspCysLysValArgValPheThrTyrIleuIleGlyArgGluVal 372
1144 AAGTACAAATTTGGCAGAGAAAGGTTTCAATCTTCACTTACCTCAATTGGACGAGAGGCT 1203
373 SerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThrGlnIle 392
1204 GCTTTTGCAGACAATCTCAAGTGGATGGCTGTGTGCTTAACAAAGATTTTTCACCCAGATC 1263
393 SerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSerArgPro 412
1264 TCCACCTTGGCTGATGTCAGGAAATATGTCATGGAATACCTCCATGTACTCGACCC 1323
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433 LeuSerSerGlnAlaGlnSerLeuThrLeuValThrValAlaMetProValPheSer 452
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493 LeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyrArgGlu 512
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2629 GGAGCTGTATGACAAAGTTGTTAAACATGGGCTCCTTTAAAGAAATAACCTTGTATGAC 2688
873 TyrGlnAlaMetCysLysProSerSerHisHisSerAlaAlaGlnProLeuValSer 892
2689 TACCAAGCCATGTGTAGACCAACAAAGGAGAGTAGTGACACTGTGCCACCGACTCTGGAC 2748
893 ProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValLeuPheLeu 912
2749 CCTATAGGCGCTTCTCTCTCGACCAAGTGGATAGTAGCAGGAACCTGTGTTGTTCTCTG 2808


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2860 -----CAGAAACTGAAACAGACACCTGGAGCCCTGTGATACTGAATACCCA 2904
Qy 953 ValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGlyProCys 972
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2905 GCCTTTGTTCCGAACGCCACCATCAAGGAGACACACAGGGAACATTGCTTGTGAAGACTGC 2964
Qy 973 GlnLysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuValThrAsp 992
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2965 TCCAAAGTCCTTTGTCATCCAGCAAAATCCCAAGTAGCAATCTGTTTCATGGTGGTGGTGAC 3024
Qy 993 ProThrCysAspCysSerIlePheProProValLeuGlnGluAlaThrGluValLysTyr 1012
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
3025 AGTAGCTGTCTCTGTGAGTCTGTGGCTCCTATCACCATGGCACCCATTGAATCAGGTAT 3084
Qy 1013 AsnAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgArgProAspSer 1032
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Qy 1033 CysHisAlaPheHisProGluValArgValGluAlaAspArgGlyTrpAlaGlyPheSer 1052
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Job time : 11579 secs

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OM protein - protein search, using sw model

Run on: November 16, 2005, 03:13:23 ; Search time 45 Seconds
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Title: US-09-833-222A-10
Perfect score: 5726
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Scoring table: BLOSUM62
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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3419.5	59.7	1077	4	US-09-397-550-24
3	3416.5	59.6	1091	4	US-10-162-012-15
4	3410.5	59.6	1065	4	US-09-397-550-12
5	3410.5	59.6	1085	4	US-09-397-550-22
6	3326.5	58.1	1038	4	US-09-397-550-11
7	3278.5	57.3	1019	4	US-09-397-550-10
8	1792.5	31.3	350	4	US-09-397-550-18
9	1695	29.6	323	4	US-09-397-550-17
10	1598	27.9	304	4	US-09-397-550-16
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17	1158.5	20.2	1082	4	US-09-397-550-5
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23	1079.5	18.9	1103	1	US-08-455-543A-53
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Sequence 25, Appl
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Sequence 4, Appl
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Sequence 54, Appl
Sequence 54, Appl
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Sequence 6, Appl
Sequence 41584, A
Sequence 100, App
Sequence 4028, Ap
Sequence 5756, Ap
Sequence 1, Appl
Sequence 3, Appl
Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-10-162-012-18
; Sequence 18, Application US/10162012
; Patent No. 6682597
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
; FILE REFERENCE: 10448-190001
; CURRENT APPLICATION NUMBER: US/10/162,012
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/209,845
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: US 09/875,321
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: PCT/US01/18340
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,423
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18398
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,238
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,363
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18247
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/227,068
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 09/928,530
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/25475
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: US 60/226,770
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/934,421
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/US01/26096
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/279,281
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 10/109,029
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: PCT/US02/09728
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/290,288
; PRIOR FILING DATE: 2001-05-11

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; PRIOR APPLICATION NUMBER: US (not assigned)
; PRIOR FILING DATE: 2002-05-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 1091
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-162-012-18

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Best Local Similarity 60.0%; Pred. No. 0;
Matches 627; Conservative 188; Mismatches 212; Indels 18; Gaps 6;

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DB 42 VKLWASAFGEIISIAAKYSGSOLLOKKYKEYEKDVAIEIDGLQLVKKLAKIMEEMFHK 101
QY 73 KVEAVQNLVEAAEADLNHEFNESLVDYVNSVLINERDEKGNFVELGAEFLLESNAHFS 132
DB 102 KSEAVRLVEAAEAEHLKHEFDADLOQYEFNAVLINERDKGNFLELGKEFILAPNDHFN 161
QY 133 NLPVNTSISSVOLPTNVYNKDPDILNGVYMSALNAVVENFORDPDLTWQYFGSATGFF 192
DB 162 NLPVNTISLSDVQVPTNMYNKDPAIVNGVYMSLSLNVFVDFNDRDPSLIWQYFGSAKGF 221
QY 193 RIYPGKWTDPENGVTTFDCRNRGWYIOAATSPKDIIVLDVSGSMKGLRMTIAKHTIT 252
DB 222 ROYPGIKWEPDENGVTAFDCRNRKWIYOAATSPKDVILVDSVSGSMKGLRLTIKQTVSS 281
QY 253 ILDTLGENDFVNIAYNDYVHYIEPCFKGILVQADRNRHEHFKLLVEELMVKGVVDOA 312
DB 282 ILDTLGDGDDFFNIITNEELHYVEPCNLGLTVQADRTNKEHFEHLDKLFAKIGMLDIA 341
QY 313 LRBAFQILKQFOBAKQSGSLCNOAIMLISDGAVDYBEPVKYKNWPCKVRVFTYLIGREV 372
DB 342 LNEAFNILSDFNHTGOGSICSAQIMLITDGAVDYDTIFAKYNWPDORVRIFTYILIGREA 401
QY 373 SPADRMKWIACNKGYYTQISTLADTOENVMYHLVLSRPMVINHDDIITWTEAYWDSKL 432
DB 402 AFADNLKMACANKGFFTOISTLADVQENVMYHLVLSRPMKVIDQEHDDVVWTEAYIDSTL 461
QY 433 LSSQA-----QSLTLTTLTVAMPVFSKKNETSRSHGILLGVVGSVDVALRELKMLAPRYKLGVH 488
DB 462 POAQKLADDQGLVMTVTAMPVFSKQNETSRSGILLGVVGTDPVKVELLKTIPYKLGIIH 521
QY 489 GYAFLNTNNGYIILSHPDRLPLREGKKLKPKNYNSVDLSEWEDEQASLRTAMINRET 548
DB 522 GYAFATITNNGYIILTHPELRPLYEEGKK-RRKPNYSVDLSEWEDEDRDDVLRNAMYNRKT 580

; PRIOR APPLICATION NUMBER: US (not assigned)
; PRIOR FILING DATE: 2002-05-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 1091
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-162-012-18

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Best Local Similarity 60.3%; Pred. No. 0;
Matches 622; Conservative 188; Mismatches 206; Indels 15; Gaps 5;

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QY 73 KVEAVQNLVEAAEADLNHEFNESLVDYVNSVLINERDEKGNFVELGAEFLLESNAHFS 132
DB 102 KSEAVRLVEAAEAEHLKHEFDADLOQYEFNAVLINERDKGNFLELGKEFILAPNDHFN 161
QY 133 NLPVNTSISSVOLPTNVYNKDPDILNGVYMSALNAVVENFORDPDLTWQYFGSATGFF 192
DB 162 NLPVNTISLSDVQVPTNMYNKDPAIVNGVYMSLSLNVFVDFNDRDPSLIWQYFGSAKGF 221
QY 193 RIYPGKWTDPENGVTTFDCRNRGWYIOAATSPKDIIVLDVSGSMKGLRMTIAKHTIT 252
DB 222 ROYPGIKWEPDENGVTAFDCRNRKWIYOAATSPKDVILVDSVSGSMKGLRLTIKQTVSS 281
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DB 282 ILDTLGDGDDFFNIITNEELHYVEPCNLGLTVQADRTNKEHFEHLDKLFAKIGMLDIA 341
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QY 373 SPADRMKWIACNKGYYTQISTLADTOENVMYHLVLSRPMVINHDDIITWTEAYWDSKL 432
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DB 462 POAQKLADDQGLVMTVTAMPVFSKQNETSRSGILLGVVGTDPVKVELLKTIPYKLGIIH 521
QY 489 GYAFLNTNNGYIILSHPDRLPLREGKKLKPKNYNSVDLSEWEDEQASLRTAMINRET 548
DB 522 GYAFATITNNGYIILTHPELRPLYEEGKK-RRKPNYSVDLSEWEDEDRDDVLRNAMYNRKT 580
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Qy	727	SVFTLDRPEFLWYRCASHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAA	786
Db	759	NIFWADHPFLWYRRAAQIPGSFVYISIPFSTGP--VNKSNVVVTASTSIQLLDERKSPVA	816
Qy	787	AAGVQMKLEFLQRKFWAATQCSVTDGPGYVTSQSCEDSDLDGCFVINDNNGFILISKRSRETR	846
Db	817	AVGIQMKLEFFQKRFWTAHQASLDGKCSISCDDETVNVCYLIDNNGFLLVSEDYDTQGD	876
Qy	847	PLGEVDGAVLTQLLSMGVFGQVWYDYQAMCKSPSSHHSAAQPLVSPISAPLATRWLLQ	906
Db	877	FFGIEGAVNKKLLTMGSSFKRITLYDYQAMCRANKESSDGAHGLLDYPNAFLSAVKWIMT	936
Qy	907	ELVLFLLEWSVWGSWYDRGAEAKSVFHHSHKHKQDFLQPCDTEYPVYVQPAIREANGI	966
Db	937	ELVLFLVEFNLC-SWHSMDMTAKA-----QKLQKTFEPCDTEYPFAVSERTIKETGNN	988
Qy	967	VEGCPCKQVFWVQOQIPNSNLLLLLVTDPTCDCSIPPPVQEBATEVKYVNASVKCDRMRSQKL	1026
Db	989	IACEDCSKSFVQIQIPSNLFMVVVDSSCLICESVAPITMAPIEIRYNESLKCBRLKAQKI	1048
Qy	1027	RRRPDSCHAFHPE	1039
Db	1049	RRRPESCHGFHPE	1061

RESULT 4

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US-09-397-550-12
; Sequence 12, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCE: 180
; CURRENT APPLICATION NUMBER: US/09/397,550
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 1065
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-397-550-12

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Qy	373	SPADRMKIACNNKGYVTOJLSTLADTOENYMEYLHVLRSRPMVINHHDDILWTAYMDSKL	432
Db	402	AFADNLKWKACANKGFFQJLSTLADQVENYMEYLHVLRSRPVJLQDEHDVVMVTEBAYIDSTL	461
Qy	433	LSSQAQSLTLITTVAMPVFSKQNETRSHGILLGVGSDVALRBLMKLAPRYKLGVHGAYF	492
Db	462	TDDQGP--VLMTTVAMPVFSKQNETRSGILLGVGVDVFPVKELLKTIIPKYLGIGHYAF	519
Qy	493	LNTNNGVILSHPDRLPIRYRGKKLKPKNYNSVDLSSEVEHQDAESLRTAMINRETCGLS	552
Db	520	AITNNGYILTHPELRLLLYEBGKK--RRKPNYSYSDVLSSEVEHQDDVLLRNAMVNRKTGKFS	578
Qy	553	MDVKVPMDKGRVLFLTNDYFFDTISDTPESLGAVALSRGHGEYVILLGNSTSVESGLDHLH	612
Db	579	MEVKTVDKGRVLVMTNDIYYTIDIKGTPESLGAVALSRGHGKTFFRGNVTIEGLHDLH	638
Qy	613	PDALAGDWITCYTIDDPDRHKLSOLEAMIRFLTRKDPDLCEDEELVREYVLFDAVVTPM	672
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Qy	673	EAYWTALALNNSESESHVVDMAFLGTRAGLLRSSLFGSEKVSDRKFLTPEDASVPTLD	732
Db	699	EAYWTSIALNKSNSDKGVEAVFLGTRTGLSRINLFGAEQLTNQDFLAKAGDKENIFNAD	758
Qy	733	RFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMWVTASTAVAVTVDKRTAIAAAAQVQM	792
Db	759	HFPLWYRRAAEQJPGSFVYSIPFSTGP--VNKSNVVTASTSIQLDERKSPVVAAVGIOM	816
Qy	793	KLBFLOKRWAAATQCSTVDGPPYTQSCESDLDLDCFVIDNNGFTILISKRSRETGRFLGEVD	852
Db	817	KLBFQKRPWTAQKQACSLDGKCSISCDDETVCYLIDNNGFTILVSEDVYQTQDGFGEIE	876
Qy	853	GAVLTQLLSCNGVFSQVMTDYQAMCKPSSHHSHAAQPLVSPISAFLTATRWLLQELVFL	912
Db	877	GAVNKLTLTNGSPKRTILTDYQAMCRANKESDGAHGLLDLPYNAFLSAVKWIMTELVLFL	936
Qy	913	LEWSVNGSYDRGAEAKEVPHSHSHKHKKODPLQPCDTEYPVFVYQPAIREANGIVECGPC	972
Db	937	VENLCL-SWVHSDMTAKA-----QKLQTEPCDTEYPAFVSERTIKETTGNIACEDC	988
Qy	973	QKVFVYVQIQPNLNLTLVTDPTCDSCIFPPVLQEADEVKYNASVKCDMRMSQKLRRRPDS	1032
Db	989	SKSFVYQIQPNLNLFWVVDSSCLCESVAPITWAPIEIRYNESLCKERLKAQKIRRPES	1048
Qy	1033	CHAPHPE 1039	
Db	1049	CHGFHPE 1055	
RESULT 5			
US-09-397-550-22			
; Sequence 22, Application US/09397550			
; Patent No. 6783952			
; GENERAL INFORMATION:			
; APPLICANT: Warner-Lambert			
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2			
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and			
; TITLE OF INVENTION: screening assays using same			
; FILE REFERENCE: 180			
; CURRENT APPLICATION NUMBER: US/09/397,550			
; CURRENT FILING DATE: 1999-09-16			
; NUMBER OF SEQ ID NOS: 28			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 22			
; LENGTH: 1085			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-09-397-550-22			

Query Match		59.6%; Score 3410.5; DB 4; Length 1085;
Best Local Similarity		60.3%; Pred. No. 0;
Matches		619; Conservative 188; Mismatches 207; Indels 13; Gaps 5;
Qy	13	VKLWADTFGGDLVNTVTYKSGSLLQKKYKDVSSLLKIEBVDGLVLRKSEDMENMLRR 72
Db	42	VKLWASAFGEIISIAAKYSGSLLQKKYKEYEKDVAIEIDGLQVLKLAKNMEFHK 101
Qy	73	KVEAVQNVLVEAAEADLNHEFNEBSLVFYNSVLINERDEKGNFVELGAEFLLESNAHFS 132
Db	102	KSEAVRRLVEAAEBAHLKHEFDADLQYEFNAVLINERDKGNFLELGKSFILAPNDHFN 161
Qy	133	NLPVNTSISSVQLPTNVYKDPDILNGVYVSEALNAVVENFQDRDPTLTWQYFGSATGFF 192
Db	162	NLPVNTSLSDVQVPTMYNKDPAIVNGVYVSESLNKVFDNFDPSLIWQYFGSAKGF 221
Qy	193	RIYPGKWTDPENGVIPTFCRNRGWYIQAAATSPKDIIVILVDVSGSMKGLRMTAKHTTT 252
Db	222	RQYPGIKWEPDENGVIATFCRNRKWIYQAATSPKDVILVDVSGSMKGLRLTTAKQTSS 281
Qy	253	ILDTLGENDFVNIAYNDYVHYIEPCFGKILVQADRNRHEFKLLVBEELMVGKGVVDQA 312
Db	282	ILDTLGDDDFNIIAYNEELHYVEPCNLGTLVQADRTNKEHFREHLDKLFAKGIGMLDIA 341
Qy	313	LREAFQILKQFQAKQSGSLCNQAIMLISDGAVEDYEPVEKYNWPCVKRVFTYLIGREV 372
Db	342	LNEAFNLSDFNHTGGSGISCSQAIMLITDGAVDYDTIFAKYNWPDVKRIFTYLIIGREA 401
Qy	373	SPADRMKWIACNNKGYTQISTLADTQENVMYELHVLSPRMVINHDHDIITWEAYMDSKL 432
Db	402	AFADNLKWMACANKGFFQTQISTLADVQENVMYELHVLSPRKVIDQEHVVWTEAYIDSTL 461
Qy	433	LSSQAQSLTLTTVAMPVFSKQNETRSKGLLGWGSVDVALRMLKAPRYKLGVHGYAF 492
Db	462	TDQGP--VLMTTVAMPVFSKQNETRSKGLLGWGTDPVVKELTKTIPKYKLGIHGYAF 519
Qy	493	LNTNNGYILSHDPLRPLRYEGKKLKPKNYNSVDLSEVEDQAESLRMTAMINRETGTL 552
Db	520	AITNNGYILTHPELRLLYBEGKK--RRKNPYSSVDLSEVEDRDDLVRNANVRKTKGFS 578
Qy	553	MDVKVPMDKGRVFLFTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVBGLDHLH 612
Db	579	MEVKTVDKGRVLMVMTNDIYYTDIKGTPTPSLGVALSRGHGKFFFRGNVTIEBGLHDLH 638
Qy	613	PDALAGDWTYICITDIDPHRKLSQLAMIRFLTRKDPDLECEBELVREYLFDAVVTAPM 672
Db	639	PDVSLADEWSYCNLDLHPEHRHLSQLEAKLYLKKGKPELLQCDKELIQEVLFDAVVSAPI 698
Qy	673	EAYWTALANMSESESHVVDMAFLGTRAGLLRSSSLFVGSEKVSDDRFLPEDEASVFTLD 732
Db	699	EAYWTSIALNKSNSDKGVEVAFGLTRTGLSRINLFGABQLTNQDPLKAGDKENIFNAD 758
Qy	733	RPLWYRQASEHPAGSPVFNLRWABGESAGEPMVYTTASTAVTVTDKRTAIAAAGVOM 792
Db	759	HFPLWYRAAEQIPGSEVYIPISTGP--VNKSNVVTASTSIQLDERKSPVVAAGIQM 816
Qy	793	KLBFLOKFWAARTQCSVDGPYTSQCEDSLDCFVIDNNGFILLISRSRETRGFLGEVD 852
Db	817	KLFEFFQKFTASRQCASLDGKCSISCDDETVCYLLDNNGFILVSEDYTQTGDFGGEIE 876
Qy	853	GAVLTQLLNGVFSQVMTYDQAMCKPSSHHSAAQLVSPISAFLTATRWLLOELVFL 912
Db	877	GAVNKLTLWGSFKRITFLYDQAMCRANKSSSDGAHGLLDPYNAFLSAVAKWIMTELVLFL 936
Qy	913	LEWSVMSGWDYRGAEAKSVFHHSHKHKQDPLQPCDTEYFVYVQPAIREANGIVEGCP 972
Db	937	VEFNLC--SWHSDMTAKA-----QKLQOTLEPCDTEYFPAFVSERTIKETTGNACEDC 988
Qy	973	QKVFVVOQIIPNSNLLLVTDPTDCSIFPPVLOEATEVKYNASVKCDMRMSQKLRRPDS 1032
Db	989	SKSFVIOQIPSSNLFMVVDSSCLCESVAPITWAPIEIRYNESLKERLKAQKIRRPES 1048
Qy	1033	CHAFHPE 1039

Db	1049	CHGFHPE 1055
RESULT 6		
US-09-397-550-11		
; Sequence 11, Application US/09397550		
; Patent No. 6783952		
; GENERAL INFORMATION:		
; APPLICANT: Warner-Lambert		
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2		
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and		
; TITLE OF INVENTION: screening assays using same		
; FILE REFERENCE: 180		
; CURRENT APPLICATION NUMBER: US/09/397,550		
; CURRENT FILING DATE: 1999-09-16		
; NUMBER OF SEQ ID NOS: 28		
; SOFTWARE: PatentIn Ver. 2.1		
; SEQ ID NO 11		
; LENGTH: 1038		
; TYPE: PRT		
; ORGANISM: Homo sapiens		
US-09-397-550-11		
Query Match		
Best Local Similarity		
Matches		
Score 3326.5; DB 4; Length 1038;		
Pred. No. 0;		
Mismatches 206; Indels 13; Gaps 5;		
Qy	13	VKLWADTFGGDLVNTVTYKSGSLLQKKYKDVSSLLKIEBVDGLVLRKSEDMENMLRR 72
Db	42	VKLWASAFGEIISIAAKYSGSLLQKKYKEYEKDVAIEIDGLQVLKLAKNMEFHK 101
Qy	73	KVEAVQNVLVEAAEADLNHEFNEBSLVFYNSVLINERDEKGNFVELGAEFLLESNAHFS 132
Db	102	KSEAVRRLVEAAEBAHLKHEFDADLQYEFNAVLINERDKGNFLELGKSFILAPNDHFN 161
Qy	133	NLPVNTSISSVQLPTNVYKDPDILNGVYVSEALNAVVENFQDRDPTLTWQYFGSATGFF 192
Db	162	NLPVNTSLSDVQVPTMYNKDPAIVNGVYVSESLNKVFDNFDPSLIWQYFGSAKGF 221
Qy	193	RIYPGKWTDPENGVIPTFCRNRGWYIQAAATSPKDIIVILVDVSGSMKGLRMTAKHTTT 252
Db	222	RQYPGIKWEPDENGVIATFCRNRKWIYQAATSPKDVILVDVSGSMKGLRLTTAKQTSS 281
Qy	253	ILDTLGENDFVNIAYNDYVHYIEPCFGKILVQADRNRHEFKLLVBEELMVGKGVVDQA 312
Db	282	ILDTLGDDDFNIIAYNEELHYVEPCNLGTLVQADRTNKEHFREHLDKLFAKGIGMLDIA 341
Qy	313	LREAFQILKQFQAKQSGSLCNQAIMLISDGAVEDYEPVEKYNWPCVKRVFTYLIGREV 372
Db	342	LNEAFNLSDFNHTGGSGISCSQAIMLITDGAVDYDTIFAKYNWPDVKRIFTYLIIGREA 401
Qy	373	SPADRMKWIACNNKGYTQISTLADTQENVMYELHVLSPRMVINHDHDIITWEAYMDSKL 432
Db	402	AFADNLKWMACANKGFFQTQISTLADVQENVMYELHVLSPRKVIDQEHVVWTEAYIDSTL 461
Qy	433	LSSQAQSLTLTTVAMPVFSKQNETRSKGLLGWGSVDVALRMLKAPRYKLGVHGYAF 492
Db	462	TDQGP--VLMTTVAMPVFSKQNETRSKGLLGWGTDPVVKELTKTIPKYKLGIHGYAF 519
Qy	493	LNTNNGYILSHDPLRPLRYEGKKLKPKNYNSVDLSEVEDQAESLRMTAMINRETGTL 552
Db	520	AITNNGYILTHPELRLLYBEGKK--RRKNPYSSVDLSEVEDRDDLVRNANVRKTKGFS 578
Qy	553	MDVKVPMDKGRVFLFTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVBGLDHLH 612
Db	579	MEVKTVDKGRVLMVMTNDIYYTDIKGTPTPSLGVALSRGHGKFFFRGNVTIEBGLHDLH 638
Qy	613	PDALAGDWTYICITDIDPHRKLSQLAMIRFLTRKDPDLECEBELVREYLFDAVVTAPM 672
Db	639	PDVSLADEWSYCNLDLHPEHRHLSQLEAKLYLKKGKPELLQCDKELIQEVLFDAVVSAPI 698
Qy	673	EAYWTALANMSESESHVVDMAFLGTRAGLLRSSSLFVGSEKVSDDRFLPEDEASVFTLD 732

Db 699 EAYWTSALNKSSENSDKGEVAFGLTRTGLSRINLFGAEQLTNQDFLKAGDKENIPNAD 758
Qy 733 RFPLMYRQAESEHPAGSFVFNLRWAESEAGPMVVTASTAVAVTVDRKRTAIAAAAGVQM 792
Db 759 HFPLMYRRAAEQIPGSEVYISPFSTGP- -VNKSNVVTASTSIQLLDERKSPVVAAGVQM 816
Qy 793 KLEFLQRKFWAATRQCSFVDPGPTQSCDSDLDGCFVDDNNGFLLISKRSETGRFLGEVD 852
Db 817 KLEFFQRKFWTASRQACASLGKCSISCDDETVCNLCYLLDNNGFILVSEDTYQTGDFGGEIE 876
Qy 853 GAVLTQLLSNGVFSQVMTYDYQAMCKPSSHHSAAQPLVSPISAFLTATRWLLQELVLFL 912
Db 877 GAVMKNLLTWSFKRITLYDYQAMCRANKESSDGAHGLDPPYNAFLSAVKWIMTELVLFL 936
Qy 913 LEWSVMSWYDRGAESVHHSHKHKQDPLQPCDTEYFVFPYQPAIREANGIVECGPC 972
Db 937 VEFNLC- -SMWHSMDTAKA- -QKQKOTLEPCDTEYPAFVSERTIKETTGNACEDC 988
Qy 973 QKVFVVOQIPNSNLLLVTDPTDCSIFPPVLOEATKVNASVKCDRMR 1022
Db 989 SKSFVIQIIPSSNLFMVVVDSSCLCESVAPIWAPIEIRNESLKCERLX 1038
RESULT 7
US-09-397-550-10
; Sequence 10, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCE: 180
; CURRENT APPLICATION NUMBER: US/09/397,550
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 1019
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-397-550-10

Query Match 57.3%; Score 3278.5; DB 4; Length 1019;
Best Local Similarity 60.4%; Pred. No. 2.9e-315; Mismatches 200; Indels 13; Gaps 5;
Matches 599; Conservative 179; Gaps 13; Indels 13; Gaps 5;
Qy 13 VKLWADTFGGDLTYNTVTYKSGSLLQKKYKDVESLKIIEVDGLVLRKFSDEMNNLRR 72
Db 42 VKLWASAFGGEIKSIAAKYSGSOLLQKKYKEYEKDVAIEIDGLQLVKLAKNWEEMPHK 101
Qy 73 KVAQVNLVBAEADLNHFENSLVFDYNSVLINERDEKGNFVGLGAFLLLESNAHFS 132
Db 102 KSEAVRRLVBAEBAHLKHEFDLQVYEFNAVLINERDKDGNFLGKGFILAPNDHFN 161
Qy 133 NLPNNTSISVOLPTVYNNKDPDLNGVYMSALNAVVENFORDPLTLWQVFGSATGPF 192
Db 162 NLPNLSLSVQVPTTNNKDPALVNGVYMSLSNKFVDFNDRDPSLIWQVFGSARGF 221
Qy 193 RIYPGKWTDPDNGVITFCRNRGWIQAATSFKDVIILVDVSGSMKGLRMTIAKTIIT 252
Db 222 RQYPGIKWEPDENGVIADFRCNRKWIQAATSFKDVIILVDVSGSMKGLRLTIKQTVSS 281
Qy 253 ILDTLGENDFWNIIANDYVHYIYEPGFKGLLVQADRNRHFKLLVEELMVKGVGVDQA 312
Db 282 ILDTLGDGDDFFNIAYNEELHYEPCPLNGTLVQADRNTKEHFEHDLKLFAGKIGMLDIA 341
Qy 313 LREAFOILKQFOBAKOGSLCNOAIMLISDGAVEDYEPVPEKYNWPKVRYFTYLLIGREV 372
Db 342 LNEAFNLSDFNHTGGQSCISQAIMLITDGAVDYDTIFAKYNWPRKWRIFTYLLIGREA 401
Qy 373 SFADRMKIACNNKGYTYTQISTLADTQENVMYHLVLSRPMVINHDHDIITWEAYMDSKL 432

Db 402 AFADNLKMWACANKGFFQISTLADYQENVMYHLVLSRPKVIDQEDHVVWTEAYIDSTL 461
Qy 433 LSSQAOSLTLITTVAMPVTSKQNETRSHGILLGVGSDVALRELKMLAPRYKLGVGHYAF 492
Db 462 TDQGGP- -VLMTTVAMPVTSKQNETRSHGILLGVGSDVALRELKMLAPRYKLGVGHYAF 519
Qy 493 LNTNNGYIILSHPDRLRPLYREGKKLKPKNVNSVDLSEVEWEDQAESLRRTAMINRETGTL 552
Db 520 AITNNGYIILTHPELRLLYEGKK- -RRKPNYSSVDLSEVEWEDRDDVLNRNANWNRKTKFS 578
Qy 553 MDVKVPMDKGRVFLFTNDYFFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEBGLDHLH 612
Db 579 MEVKTKVDGKRVLMTNDYVYVTDIKGTPFSLGVALSRGHGKYFFRGNVTIESGLHDLB 638
Qy 613 POLALAGDWIYCIITDDPHRKLSQLBAMIRFLTRKDPDLECEBELVREVLFDAVVTAPM 672
Db 639 PDVSLADEWSYCNVTDLHPEHRLSQLBAMIRFLTRKDPDLECEBELVREVLFDAVVTAPM 698
Qy 673 EAYWTALANMSESESHVVDMAFLGTRAGLLRSSLFVSGSEKVSDDRFLTPEDASVFTLD 732
Db 699 EAYWTSALNKSSENSDKGEVAFGLTRTGLSRINLFGAEQLTNQDFLKAGDKENIPNAD 758
Qy 733 RFPLMYRQAESEHPAGSFVFNLRWAESEAGPMVVTASTAVAVTVDRKRTAIAAAAGVQM 792
Db 759 HFPLMYRRAAEQIPGSEVYISPFSTGP- -VNKSNVVTASTSIQLLDERKSPVVAAGVQM 816
Qy 793 KLEFLQRKFWAATRQCSFVDPGPTQSCDSDLDGCFVDDNNGFLLISKRSETGRFLGEVD 852
Db 817 KLEFFQRKFWTASRQACASLGKCSISCDDETVCNLCYLLDNNGFILVSEDTYQTGDFGGEIE 876
Qy 853 GAVLTQLLSNGVFSQVMTYDYQAMCKPSSHHSAAQPLVSPISAFLTATRWLLQELVLFL 912
Db 877 GAVMKNLLTWSFKRITLYDYQAMCRANKESSDGAHGLDPPYNAFLSAVKWIMTELVLFL 936
Qy 913 LEWSVMSWYDRGAESVHHSHKHKQDPLQPCDTEYFVFPYQPAIREANGIVECGPC 972
Db 937 VEFNLC- -SMWHSMDTAKA- -QKQKOTLEPCDTEYPAFVSERTIKETTGNACEDC 988
Qy 973 QKVFVVOQIPNSNLLLVTDPTDCSIFPPV 1003
Db 989 SKSFVIQIIPSSNLFMVVVDSSCLCESVAPI 1019
RESULT 8
US-09-397-550-18
; Sequence 18, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCE: 180
; CURRENT APPLICATION NUMBER: US/09/397,550
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-397-550-18
Query Match 31.3%; Score 1792.5; DB 4; Length 350;
Best Local Similarity 97.4%; Pred. No. 1.2e-168;
Matches 341; Conservative 2; Mismatches 6; Indels 1; Gaps 1;
Qy 700 AGLLRSSILFVSGSEKVSDDRFLTPEDASVFTLDRLPPLWYRQASEHPAGSFVFNLRWAEGP 759
Db 1 SGLLRSSILFVSGSEKVSDDRFLTPEDASVFTLDRLPPLWYRQASEHPAGSFVFNLRWAEGP 60
Qy 760 ESAGEPMVVTASTAVAVTVDRKRTAIAAAAGVQMKLEFLQRKFWAATRQCSVTDGPTQSC 819

Db 61 ESAGEPMVVTASTAVAVTVDKRTAIAAAGVQMKLEFLQRFKFWAATRCQSTVDGPTQSC 120
Qy 820 EDSLDLCFVIDNNGFILISKRSRETGRFLGEVDGAVLTQLLSMGVFSQVTMYDYQAMCKP 879
Db 121 EDSLDLCFVIDNNGFILISKRSRETGRFLGEVDGAVLTQLLSMGVFSQVTMYDYQAMCKP 180
Qy 880 SSHHSAAPLVSPISAFATATRWLLQELVLFLEWSVMSGYDRGAEAHSVHHSHKHK 939
Db 181 SSHHSAAPLVSPISAFATATRWLLQELVLFLEWSVMSGYDRGAEAHSVHHSHKHK 240
Qy 940 KQDPLQPCDTEYFVYVQPAIREANGIVEGCPCKVFWVQOIPNSNLLLLVTPDTCDCSI 999
Db 241 KQDPLQPCDTEYFVYVQPAIREANGIVEGCPCKVFWVQOIPNSNLLLLVTPDTCDCSI 300
Qy 1000 FPPVLQATEVKYNASVKCDRMRSQLRRRDPDSCHAFHPEVRVEADRGWA 1049
Db 301 FPPVLQATEVKYNASVKCDRMRSQLRRRDPDSCHAFHPEVNAQ-DCGGA 349

RESULT 9
US-09-397-550-17
; Sequence 17, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCE: 180
; CURRENT APPLICATION NUMBER: US/09/397,550
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-397-550-17

Query Match 29.6%; Score 1695; DB 4; Length 323;
Best Local Similarity 99.4%; Pred. No. 4.9e-159;
Matches 321; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 700 AGLRSSLFVSGSEKVS DRKFLTPEDASVFTLDRFPFLWYRQASEHPAGSFVFNLRWAE GP 759
Db 1 SGLRSSLFVSGSEKVS DRKFLTPEDASVFTLDRFPFLWYRQASEHPAGSFVFNLRWAE GP 60
Qy 760 ESAGEPMVVTASTAVAVTVDKRTAIAAAGVQMKLEFLQRFKFWAATRCQSTVDGPTQSC 819
Db 61 ESAGEPMVVTASTAVAVTVDKRTAIAAAGVQMKLEFLQRFKFWAATRCQSTVDGPTQSC 120
Qy 820 EDSLDLCFVIDNNGFILISKRSRETGRFLGEVDGAVLTQLLSMGVFSQVTMYDYQAMCKP 879
Db 121 EDSLDLCFVIDNNGFILISKRSRETGRFLGEVDGAVLTQLLSMGVFSQVTMYDYQAMCKP 180
Qy 880 SSHHSAAPLVSPISAFATATRWLLQELVLFLEWSVMSGYDRGAEAHSVHHSHKHK 939
Db 181 SSHHSAAPLVSPISAFATATRWLLQELVLFLEWSVMSGYDRGAEAHSVHHSHKHK 240
Qy 940 KQDPLQPCDTEYFVYVQPAIREANGIVEGCPCKVFWVQOIPNSNLLLLVTPDTCDCSI 999
Db 241 KQDPLQPCDTEYFVYVQPAIREANGIVEGCPCKVFWVQOIPNSNLLLLVTPDTCDCSI 300
Qy 1000 FPPVLQATEVKYNASVKCDRMR 1022
Db 301 FPPVLQATEVKYNASVKCDRMR 323

RESULT 10
US-09-397-550-16
; Sequence 16, Application US/09397550
; Patent No. 6783952

; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCE: 180
; CURRENT APPLICATION NUMBER: US/09/397,550
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-397-550-16

Query Match 27.9%; Score 1598; DB 4; Length 304;
Best Local Similarity 99.3%; Pred. No. 1.8e-149;
Matches 302; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 700 AGLRSSLFVSGSEKVS DRKFLTPEDASVFTLDRFPFLWYRQASEHPAGSFVFNLRWAE GP 759
Db 1 SGLRSSLFVSGSEKVS DRKFLTPEDASVFTLDRFPFLWYRQASEHPAGSFVFNLRWAE GP 60
Qy 760 ESAGEPMVVTASTAVAVTVDKRTAIAAAGVQMKLEFLQRFKFWAATRCQSTVDGPTQSC 819
Db 61 ESAGEPMVVTASTAVAVTVDKRTAIAAAGVQMKLEFLQRFKFWAATRCQSTVDGPTQSC 120
Qy 820 EDSLDLCFVIDNNGFILISKRSRETGRFLGEVDGAVLTQLLSMGVFSQVTMYDYQAMCKP 879
Db 121 EDSLDLCFVIDNNGFILISKRSRETGRFLGEVDGAVLTQLLSMGVFSQVTMYDYQAMCKP 180
Qy 880 SSHHSAAPLVSPISAFATATRWLLQELVLFLEWSVMSGYDRGAEAHSVHHSHKHK 939
Db 181 SSHHSAAPLVSPISAFATATRWLLQELVLFLEWSVMSGYDRGAEAHSVHHSHKHK 240
Qy 940 KQDPLQPCDTEYFVYVQPAIREANGIVEGCPCKVFWVQOIPNSNLLLLVTPDTCDCSI 999
Db 241 KQDPLQPCDTEYFVYVQPAIREANGIVEGCPCKVFWVQOIPNSNLLLLVTPDTCDCSI 300
Qy 1000 FPPV 1003
Db 301 FPPV 304

RESULT 11
US-09-470-443-6
; Sequence 6, Application US/09470443
; Patent No. 6441156
; GENERAL INFORMATION:
; APPLICANT: Leiman, Michael I.
; APPLICANT: Minna, John D.
; APPLICANT: Latif, Farida
; APPLICANT: Wei, Ming-Hui
; APPLICANT: Sekido, Yoshitaka
; APPLICANT: Gao, Boning
; APPLICANT: Duh, Fuh-Mei
; TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof
; FILE REFERENCE: NIH-05043
; CURRENT APPLICATION NUMBER: US/09/470,443
; CURRENT FILING DATE: 1999-12-22
; EARLIER APPLICATION NUMBER: 60/114,359
; EARLIER FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1076
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-470-443-6

Query Match 20.7%; Score 1183.5; DB 4; Length 1076;
Best Local Similarity 29.6%; Pred. No. 2.7e-107;

Db 533 DIKRLTNYTGANGYVFAIDLNGYVLLHPLNPKQTNTNPREPVTL-----DFLDAE 583
Qy 532 WEDQ-ABSLRTAMINRETGTLSMDVKVPMKGRKRVFLTNDYFPTDTSDFPFLSGAVLSR 590
Db 584 LEDENKEEIRSMIDGNKGKHQIRTLVKSLDRIYDEVTRNYTWVPRSTNYSGLVLP 643
Qy 591 GHGEYI-----LLGNTSVBEGUHLHPLDALAGDWIYICITIDDPHRK 634
Db 644 YSTFYLOANLSDQILQVKYFEFLPSSFESEG-HVFIAPR-----EYC-KOLNASDNN 694
Qy 635 LSOLEAMIRFLTRKDPD-LECDEBELVRELVDAVVTAPM-EAYWTALALNMSESEHVVD 692
Db 695 TEFUKNFIELMEKVTPOSKOCNNFLNLHLLDGTITQQLVERVWRDQDLN-----TVSLL 749
Qy 693 MAFLGTRAGLRSSLFVSGSEKVSDRKFLTPDEASVFTLDRFPL---WYRQASEHPAGSF 749
Db 750 AVFAATDGGITR-----VFNKAEDWTENPEPNASFYRRSLDN--HGY 792
Qy 750 VFN-----LRWAGP-ESAGEPMVVTASTAVAVTDKRTAIAAAAGVOMKLEFLQRF 801
Db 793 VFKPPHQDALLR-----PLELENDTVGILVSTAVELSLGRRTLPRVAVGVKLDLEAWAEKF 848
Qy 802 WAATRCSTVDGPTYQSC-----EDSLDCFVIDNNGFILLISKRSR---ETGR 846
Db 849 KVLASNRTHQDQP--QKCGPNSHCEMDCVNNEDLLCVLIDGGFLVLSNQNHQMDQVGR 906
Qy 847 FLGEVDGAVLTQLLSMGVFSQVMTYDQAMCKPSSHHSAAQP---LVSPISAPL----- 898
Db 907 FFEVDANLMLALYNNSFYTRKESYDQACAPQPPGNLGAAPRGVFPVPTVADFLNLAW 966
Qy 899 -TATRWLLQBLVFLLEWSVWGSWYDRG---ABAKSVFHHSHKHKKQDPLQPCDTETYPVF 954
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Qy 955 VYQPAITREA-NGIVECPCQKVFVQOIPNSNLLLTVD-PTCDCSIFFPVLQEAETVKY 1012
Db 1014 -YFGSVNASYNAIDCNCNRLFHAORLTNTLLFVVAEPLCSQCAGRLLOKETHCPA 1072
Qy 1013 NASVKCDRMRSQKLRRRPDSCHAFHPEVRVEADRGWAGFSNPPLCICLGLCPCRQ--EHIG 1070
Db 1073 DGEQELVORPRYRGPHICFDYN-----ATEDSDCGRGAFFPSLGLVLSQLLLLG 1128
Qy 1071 MPNMTVPVLLGNIRV 1087
Db 1129 LPPRPOQVLVHASRRL 1145

RESULT 13

US-09-470-443--4
; Sequence 4, Application US/09470443
; Patent No. 6441156
; GENERAL INFORMATION:
; APPLICANT: Lerman, Michael I.
; APPLICANT: Minna, John D.
; APPLICANT: Latif, Farida
; APPLICANT: Wei, Ming-Hui
; APPLICANT: Sekido, Yoshitaka
; APPLICANT: Gao, Boning
; APPLICANT: Duh, Fuh-Wei
; TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof
; FILE REFERENCE: NIH-05043
; CURRENT APPLICATION NUMBER: US/09/470,443
; CURRENT FILING DATE: 1999-12-22
; EARLIER APPLICATION NUMBER: 60/114,359
; EARLIER FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1145
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-470-443--4

Query Match 20.7%; Score 1183.5; DB 4; Length 1145;
Best Local Similarity 29.6%; Pred. No. 3e-107;
Matches 343; Conservative 209; Mismatches 436; Indels 169; Gaps 42;
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Qy 76 AVQNLVEAAEADLNHEFNEISLFD---YNSVLINERDE-KGNFVELGA-----EFL 124
Db 133 ALKRLADAENFQKAHRWQDNIKEEDIVVYDAKADAELDDPESEDVERGSKASTLRLDFI 192
Qy 125 LESNAHPSNLPVNTSSVOLPNVYNKDDPIINGVMSSEALNAVFNVENFQRPDPTLWQY 184
Db 193 EDPN--FKN-KVNSYAAVQIPTDIYKGSTVILNELNWTALENVFPMENRQDPTLLWQV 249
Qy 185 FGSATGFFRYPGIKWTPBENGVIPTDCRNRGWYIOAATSPKDIVILVDVSGSMKGRMT 244
Db 250 FGSATGTRYYPATPRAPKK-IDLYDVRRRPWTIOGASSPKDMVIIIVDVGSGVGLTK 308
Qy 245 IAKHTITITLDTLGENDFVNIIAYNDYVHYIEPCFGILVQADNRDREHFKLLVVEELMKV 304
Db 309 LMKTSVCEMLDTLSDDDYNNVASFNEKAQPVSCFTH-LVQANVRNKKVFKAVQGVAK 366
Qy 305 GGVVDQALREAPQILKQFOEAKQSGSLCNOAIMLSGAVEDYEPVEKYNWPDCKVRVF 364
Db 367 GTTYKAGPEYAPDQLQNSNITRAN--CNKIMMFTDGGEDRVQDVFEKYNWPNRTVRVF 424
Qy 365 TYLIGREVFSADRMKMIACNNKGYTYQISTLATQENWMEYLHVLSPMWI--NHDHDI 422
Db 425 TFSVGQHNVDVTPLOMACANKGYFEIPISGAIRINTQYLDVLRGPMVLAKGAKQVQ 484
Qy 423 WTEAYMDSKLLSQAQSLTLTTVAMPVFS-----KKNETRSHGILLGVGSDVALR 474
Db 485 WTNVYED-----ALGLGLVVTGTLVPENLTODGPEKQKQ-----LILGVMGIDVALN 532
Qy 475 ELMKLAIRYKLGWHGVAFLNTNGYILSHPDRLPL---YREGKKLKPKNYNSVDLSEVE 531
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Qy 532 WEDQ-AESLRTAMINRETGTLSMDVKVPMKGRKRVFLTNDYFPTDTSDFPFLSGAVLSR 590
Db 584 LEDENKEEIRSMIDGNKGKHQIRTLVKSLDRIYDEVTRNYTWVPRSTNYSGLVLP 643
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Qy 635 LSOLEAMIRFLTRKDPD-LECDEBELVRELVDAVVTAPM-EAYWTALALNMSESEHVVD 692
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Qy 693 MAFLGTRAGLRSSLFVSGSEKVSDRKFLTPDEASVFTLDRFPL---WYRQASEHPAGSF 749
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Qy 750 VFN-----LRWAGP-ESAGEPMVVTASTAVAVTDKRTAIAAAAGVOMKLEFLQRF 801
Db 793 VFKPPHQDALLR-----PLELENDTVGILVSTAVELSLGRRTLPRVAVGVKLDLEAWAEKF 848
Qy 802 WAATRCSTVDGPTYQSC-----EDSLDCFVIDNNGFILLISKRSR---ETGR 846
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Qy 847 FLGEVDGAVLTQLLSMGVFSQVMTYDQAMCKPSSHHSAAQP---LVSPISAPL----- 898
Db 907 FFEVDANLMLALYNNSFYTRKESYDQACAPQPPGNLGAAPRGVFPVPTVADFLNLAW 966
Qy 899 -TATRWLLQBLVFLLEWSVWGSWYDRG---ABAKSVFHHSHKHKKQDPLQPCDTETYPVF 954
Db 967 TSAAAWSLFQQLLYGL---IYHSWFQADPAEAGSPETRESSCVMKQ-----TQY--- 1013

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 QY 1071 MPMTTPVPLLGNIRV 1087
 Db 1129 LPPRPQPVLVHASRRL 1145

RESULT 14
 US-09-397-550-20
 ; Sequence 20, Application US/09397550
 ; Patent No. 6783952
 ; GENERAL INFORMATION:
 ; APPLICANT: Warner-Lambert
 ; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
 ; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
 ; TITLE OF INVENTION: screening assays using same
 ; FILE REFERENCE: 180
 ; CURRENT APPLICATION NUMBER: US/09/397,550
 ; CURRENT FILING DATE: 1999-09-16
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 20
 ; LENGTH: 1145
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-397-550-20

Query Match 20.7%; Score 1183.5; DB 4; Length 1145;
 Best Local Similarity 29.6%; Pred. No. 3e-107;
 Matches 343; Conservative 209; Mismatches 436; Indels 169; Gaps 42;

QY 16 WADTGGDLYNTVTKYSGSLLOKVKYVSSLLKIEVDGLVLRKFSDEMNLRRKVE 75
 Db 73 WARRLEQEVGDMVIRFGVQQLREIYKDNRLFEVQENEPQKLVEKVGADIESLLDRKVQ 132
 QY 76 AVQNLVEAAEADLNHFNESLFD---YNSVLINERDE-KGNFVELGA-----EFL 124
 Db 133 ALKRLADAENFQKAHRWQDNKEEDIVVYDADAELDPEDSEDVERGSKASTLRDLFI 192
 QY 125 LESNAHFNPLVNTSSVOLPTNVNKPDIINGVYMSEALNAVFNENFQRPDTLTWQY 184
 Db 193 EDPN--FKN-KVNSYAAVQIPTDIYKGSTVILNLTWLEALNSVFMENRRQDPTLLWQV 249
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 Db 250 FGSATGVTRYYPATPRAPKK-TLDVDRRPPHYIOGASSPKDMVILVDVSGSVGLTK 308
 QY 245 IAKHTITLDTLIGENDFVNIAYNDVHYIEPCFKGILVQADRDNRHFKLVEBLMKV 304
 Db 309 LMKTSVCEMLDTLSDDDYNNVASFNEKAQPV-S-CFTH-LVQAVNRKKVFKZAVQGVAK 366
 QY 305 GUGVVDQALBEAQILKQFEAQKQSLCNOAIMLISDGAVEDYEPFEKYNWPDCKRVF 364
 Db 367 GTTYGKAGFEYAFDQLNSNITRAN--CNKIMMFTDGGEDRVQDVFEEKYNWPNRTVRVF 424
 QY 365 TYLIGEVSPADRMKVIACNNKGYTYTQISTLATQENVMYELHLVSRPMVI--NHDHDI 422
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 QY 591 GHGEYI-----LLGNTSVVEGLHLLHPDLALAGDWIYCIITDIDPDHRK 634
 Db 644 YSTFYLOANLSDQILQVKYFEFLPSSFSEG-HVFIAPR-----EYC-KOLNASDNN 694
 QY 635 LSQLEAMIRFLTRKDPD-LECDDELVREVLFDVAVTAPM-EAYWTALALNMSSESHVVD 692
 Db 695 TEFKNFIBELMEKVTDPDKOCNNFLHNLIDTGTITQQLVERVMRQDLDL-----TYSLL 749
 QY 693 MAPLGTAGLLRSSLFVSGSEKVSDDRFLTPDEASVFTLDRFPL---WYRQASEHPAGSF 749
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 Db 907 FPEVDANLMLALYNNISFYRKESYDYQAACAPQPGNGLGAAPRGVFPVTVADFLNLAW 966
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 Db 1073 DGPEQCELVORPRYRGPHICFDYN----ATEDTSDCGRGASFPPLSLGLVLSQLLLLG 1128
 QY 1071 MPMTTPVPLLGNIRV 1087
 Db 1129 LPPRPQPVLVHASRRL 1145

RESULT 15
 US-09-397-550-6
 ; Sequence 6, Application US/09397550
 ; Patent No. 6783952
 ; GENERAL INFORMATION:
 ; APPLICANT: Warner-Lambert
 ; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
 ; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
 ; TITLE OF INVENTION: screening assays using same
 ; FILE REFERENCE: 180
 ; CURRENT APPLICATION NUMBER: US/09/397,550
 ; CURRENT FILING DATE: 1999-09-16
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 1109
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-397-550-6

Query Match 20.6%; Score 1179.5; DB 4; Length 1109;
 Best Local Similarity 30.0%; Pred. No. 7e-107;
 Matches 332; Conservative 202; Mismatches 408; Indels 163; Gaps 40;

QY 16 WADTGGDLYNTVTKYSGSLLOKVKYVSSLLKIEVDGLVLRKFSDEMNLRRKVE 75
 Db 73 WARRLEQEVGDMVIRFGVQQLREIYKDNRLFEVQENEPQKLVEKVGADIESLLDRKVQ 132

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OM protein - protein search, using sw model

Run on: November 16, 2005, 03:22:59 ; Search time 175 Seconds
(without alignments)
2606.093 Million cell updates/sec

Title: US-09-833-222A-10
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues
Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pcp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	Query Match	Length DB ID	Description		
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2	5726	100.0	1090 14	US-10-119-624-10	Sequence 10, Appl	
3	5385.5	94.1	1207 16	US-10-128-558-176	Sequence 176, App	
4	5234.5	91.4	1075 15	US-10-257-174-34	Sequence 34, App	
5	5230.5	91.3	1114 15	US-10-257-174-35	Sequence 35, Appl	
6	3808	66.5	1310 15	US-10-357-022-12	Sequence 12, Appl	
7	3422	59.8	1091 9	US-09-875-423-5	Sequence 5, Appli	
8	3422	59.8	1091 14	US-10-162-012-18	Sequence 18, Appl	
9	3422	59.8	1091 15	US-10-162-102-18	Sequence 18, Appl	
10	3419.5	59.7	1077 17	US-10-902-531-24	Sequence 24, Appl	
11	3416.5	59.7	1091 9	US-09-875-423-2	Sequence 2, Appli	

12	3416.5	59.7	1091	14	US-10-162-012-15	Sequence 15, Appl
13	3416.5	59.7	1091	15	US-10-162-102-15	Sequence 15, Appl
14	3411	59.6	1091	17	US-10-924-081-6	Sequence 6, Appli
15	3410.5	59.6	1065	17	US-10-902-531-12	Sequence 12, Appl
16	3410.5	59.6	1085	17	US-10-902-531-22	Sequence 22, Appl
17	3410	59.6	1085	17	US-10-924-081-4	Sequence 4, Appli
18	3266.5	58.1	1038	17	US-10-902-531-11	Sequence 11, Appl
19	3278.5	57.3	1019	17	US-10-902-531-10	Sequence 10, Appl
20	3250.5	56.8	997	18	US-10-972-024-263	Sequence 263, App
21	3029.5	52.9	947	16	US-10-478-758-4	Sequence 4, Appli
22	2933	51.2	949	17	US-10-924-081-9	Sequence 9, Appli
23	2305	40.3	497	15	US-10-334-143-23	Sequence 23, Appl
24	1792.5	31.3	350	17	US-10-902-531-18	Sequence 18, Appl
25	1695	29.6	323	17	US-10-902-531-17	Sequence 17, Appl
26	1598	27.9	304	17	US-10-902-531-16	Sequence 16, Appl
27	1410	24.6	2172	20	US-11-097-143-30666	Sequence 30666, A
28	1322.5	23.1	1022	20	US-11-097-143-13494	Sequence 13494, A
29	1291	22.5	1191	20	US-11-097-143-9117	Sequence 9117, Ap
30	1189	20.8	1098	18	US-10-823-432-35	Sequence 35, Appl
31	1188	20.7	1150	17	US-10-924-081-3	Sequence 3, Appli
32	1184.5	20.7	1157	17	US-10-924-081-11	Sequence 11, Appl
33	1183.5	20.7	1076	14	US-10-116-949-6	Sequence 6, Appli
34	1183.5	20.7	1145	14	US-10-116-949-2	Sequence 2, Appli
35	1183.5	20.7	1145	14	US-10-116-949-4	Sequence 4, Appli
36	1183.5	20.7	1145	16	US-10-723-860-1799	Sequence 1799, Ap
37	1183.5	20.7	1145	17	US-10-482-029-114	Sequence 114, App
38	1183.5	20.7	1145	17	US-10-902-531-20	Sequence 20, Appl
39	1182.5	20.7	1157	17	US-10-924-081-1	Sequence 1, Appli
40	1182.5	20.7	1157	18	US-10-823-432-33	Sequence 33, Appl
41	1182.5	20.7	1157	18	US-10-823-432-34	Sequence 34, Appl
42	1182	20.6	1156	18	US-10-823-432-32	Sequence 32, Appl
43	1180	20.6	1148	18	US-10-823-432-36	Sequence 36, Appl
44	1179.5	20.6	1109	17	US-10-902-531-6	Sequence 6, Appli
45	1179.5	20.6	1115	17	US-10-902-531-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-09-833-222A-10
; Sequence 10, Application US/09833222A
; Publication No. US20030166045A1
; GENERAL INFORMATION:
; APPLICANT: Codd, Ellen
; TITLE OF INVENTION: cDNA encoding the Calcium Channel Alpha2Delta-4 Subunit
; FILE REFERENCE: calcium channel alpha2delta-4 subunit
; CURRENT APPLICATION NUMBER: US/09/833,222A
; CURRENT FILING DATE: 2001-04-01
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 1090
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-222A-10

Query Match		100.0%;	Score 5726;	DB 10;	Length 1090;
Best Local Similarity		100.0%;	Pred. No. 0;		
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			Indels	0;	Gaps
				0;	
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Db	61	KFSEDENMLRRKVEAVQNVLEAAEADLNHEFNESLVFDYVNSVLINERDEKGNFVELG	120		
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Qy 361 VRVFTYLI.GREVSFADRMKWIACNNKGYTQISTLADTQENWMEYLHVLSPRPMVINHDH 420
|
|
|
Db 361 VRVFTYLI.GREVSFADRMKWIACNNKGYTQISTLADTQENWMEYLHVLSPRPMVINHDH 420
|
|
|
Qy 421 IIWTEAYMDSKLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSVALRELMLKLA 480
|
|
|
Db 421 IIWTEAYMDSKLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSVALRELMLKLA 480
|
|
|
Qy 481 PRYKLGVHGAFINTNNGYILSHPDRLPLYREGKCLKPKPNYSVDLSSEWEDQAESLR 540
|
|
|
Db 481 PRYKLGVHGAFINTNNGYILSHPDRLPLYREGKCLKPKPNYSVDLSSEWEDQAESLR 540
|
|
|
Qy 541 TAMINRETGTL.SMDVKVPMDKGRVLF.LTNDYFFTDISTDPFSLGAVLSRGHGEYILLGN 600
|
|
|
Db 541 TAMINRETGTL.SMDVKVPMDKGRVLF.LTNDYFFTDISTDPFSLGAVLSRGHGEYILLGN 600
|
|
|
Qy 601 TSVEEGLHDLHPDLALAGDWIYCIITIDPDHRKLSOLEAMIRFLTRKOPDLCEBELVR 660
|
|
|
Db 601 TSVEEGLHDLHPDLALAGDWIYCIITIDPDHRKLSOLEAMIRFLTRKOPDLCEBELVR 660
|
|
|
Qy 661 EVLFDVAVTAPMEAYWTALANMSESESHVVDMAF.LGTRAGLLRSSLFVSGSEKVSORKFL 720
|
|
|
Db 661 EVLFDVAVTAPMEAYWTALANMSESESHVVDMAF.LGTRAGLLRSSLFVSGSEKVSORKFL 720
|
|
|
Qy 721 TPDEASVFTLDRFPLWYRQASEHPAGSFVNLRWAEGPESAGEPMVVTASTAVAVTVDK 780
|
|
|
Db 721 TPDEASVFTLDRFPLWYRQASEHPAGSFVNLRWAEGPESAGEPMVVTASTAVAVTVDK 780
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|
|
Qy 781 RTAIAAAAGVOMKLEFLQRFKFWAATRCSTVDGPYTQSCEDSDLCFCFVIDNNGFILLISK 840
|
|
|
Db 781 RTAIAAAAGVOMKLEFLQRFKFWAATRCSTVDGPYTQSCEDSDLCFCFVIDNNGFILLISK 840
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|
Qy 841 SRETGRPLGEVDGAVLTOLL.SMGVFSQVTMYDYQAMCKPSSHHSAAQPLVSPISAF.LTA 900
|
|
|
Db 841 SRETGRPLGEVDGAVLTOLL.SMGVFSQVTMYDYQAMCKPSSHHSAAQPLVSPISAF.LTA 900
|
|
|
Qy 901 TRWLLQELVLF.LLEWSVWG.SWYDRGAEAKSVFHHSHKHKQDPLQPCDTEYPVFVYQPAI 960
|
|
|
Db 901 TRWLLQELVLF.LLEWSVWG.SWYDRGAEAKSVFHHSHKHKQDPLQPCDTEYPVFVYQPAI 960
|
|
|
Qy 961 REANGIVECPCQKVFVVOQI.PNSNLLLLVTDPTCDCSI.PPPVLOBATEVKYNASVKCDR 1020
|
|
|
Db 961 REANGIVECPCQKVFVVOQI.PNSNLLLLVTDPTCDCSI.PPPVLOBATEVKYNASVKCDR 1020
|
|
|
Qy 1021 MRSQKLRPRPDSCHAF.HPEVRVADRWAGFSSPNPLCLGL.CPCROEHTGMPMNTVPV.L 1080
|
|
|
Db 1021 MRSQKLRPRPDSCHAF.HPEVRVADRWAGFSSPNPLCLGL.CPCROEHTGMPMNTVPV.L 1080
|
|
|
Qy 1081 LGGNIRVYAL 1090
|
|
|
Db 1081 LGGNIRVYAL 1090
|
|
|
```

RESULT 2

US-10-119-624-10
; Sequence 10, Application US/10119624
; Publication No. US20030170785A1
; GENERAL INFORMATION:
; APPLICANT: Qin, Ning
; APPLICANT: Codd, Ellen

; TITLE OF INVENTION: cDNA Encoding a Human No. US20030170785A1el Alpha2 Delta4 Calcium
; FILE REFERENCES: ORT-1622
; CURRENT APPLICATION NUMBER: US/10/119,624
; CURRENT FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US 09/833,222
; PRIOR FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 1090
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-119-624-10

Query Match 100.0%; Score 5726; DB 14; Length 1090;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1090; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAVALGTRRRDRVKLWADTFGGDLVNTVTKYSGSLLLQKKYKDVESLSKIEEVDGLLEVR 60

Db 1 MAVALGTRRRDRVKLWADTFGGDLVNTVTKYSGSLLLQKKYKDVESLSKIEEVDGLLEVR 60

Qy 61 KFSDEMNNMLRRKVEAVQNLVEAABEADLNHBFNESLVFDYNSVLINERDEKGNFVELG 120

Db 61 KFSDEMNNMLRRKVEAVQNLVEAABEADLNHBFNESLVFDYNSVLINERDEKGNFVELG 120

Qy 121 APLLESNAHFSLNLPVNTSISSVOLPTNVNKDPDILNGVYMSEALNAVFEVFORDP.L 180

Db 121 APLLESNAHFSLNLPVNTSISSVOLPTNVNKDPDILNGVYMSEALNAVFEVFORDP.L 180

Qy 181 TWQYFGSATGFFRIYPGIKWTPDENGVIITFCRNRMWYIOAATSPKDIVILVDVSGSMKG 240

Db 181 TWQYFGSATGFFRIYPGIKWTPDENGVIITFCRNRMWYIOAATSPKDIVILVDVSGSMKG 240

Qy 241 LRMTIAKHTTITLDTLGTENDFNVIINAYNDVHYIEPCFKGILVQADRDNRHFKLLVEE 300

Db 241 LRMTIAKHTTITLDTLGTENDFNVIINAYNDVHYIEPCFKGILVQADRDNRHFKLLVEE 300

Qy 301 LMVKGVGVDOALREAFQILKQOEAKOGSLCNOAIMLI.SDGAVEDYEPVFEKYNPDCK 360

Db 301 LMVKGVGVDOALREAFQILKQOEAKOGSLCNOAIMLI.SDGAVEDYEPVFEKYNPDCK 360

Qy 361 VRVFTYLI.GREVSFADRMKWIACNNKGYTQISTLADTQENWMEYLHVLSPRPMVINHDH 420

Db 361 VRVFTYLI.GREVSFADRMKWIACNNKGYTQISTLADTQENWMEYLHVLSPRPMVINHDH 420

Qy 421 IIWTEAYMDSKLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSVALRELMLKLA 480

Db 421 IIWTEAYMDSKLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSVALRELMLKLA 480

Qy 481 PRYKLGVHGAFINTNNGYILSHPDRLPLYREGKCLKPKPNYSVDLSSEWEDQAESLR 540

Db 481 PRYKLGVHGAFINTNNGYILSHPDRLPLYREGKCLKPKPNYSVDLSSEWEDQAESLR 540

Qy 541 TAMINRETGTL.SMDVKVPMDKGRVLF.LTNDYFFTDISTDPFSLGAVLSRGHGEYILLGN 600

Db 541 TAMINRETGTL.SMDVKVPMDKGRVLF.LTNDYFFTDISTDPFSLGAVLSRGHGEYILLGN 600

Qy 601 TSVEEGLHDLHPDLALAGDWIYCIITIDPDHRKLSOLEAMIRFLTRKOPDLCEBELVR 660

Db 601 TSVEEGLHDLHPDLALAGDWIYCIITIDPDHRKLSOLEAMIRFLTRKOPDLCEBELVR 660

Qy 661 EVLFDVAVTAPMEAYWTALANMSESESHVVDMAF.LGTRAGLLRSSLFVSGSEKVSORKFL 720

Db 661 EVLFDVAVTAPMEAYWTALANMSESESHVVDMAF.LGTRAGLLRSSLFVSGSEKVSORKFL 720

Qy 721 TPDEASVFTLDRFPLWYRQASEHPAGSFVNLRWAEGPESAGEPMVVTASTAVAVTVDK 780

Db 721 TPDEASVFTLDRFPLWYRQASEHPAGSFVNLRWAEGPESAGEPMVVTASTAVAVTVDK 780

Qy 781 RTAIAAAAGVOMKLEFLQRFKFWAATRCSTVDGPYTQSCEDSDLCFCFVIDNNGFILLISK 840

Db 781 RTAIAAAAGVOMKLEFLQRFKFWAATRCSTVDGPYTQSCEDSDLCFCFVIDNNGFILLISK 840

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QY 841 SRETGRFLGVDGAVLTQLLSMGVFSQVTWYDYQAMCKPSSHHSAQAQPLVSPISAFITA 900
DB 841 SRETGRFLGVDGAVLTQLLSMGVFSQVTWYDYQAMCKPSSHHSAQAQPLVSPISAFITA 900
QY 901 TRWLLQELVLFLLWSVWGSWYDRGAESVFFHSHKHKKODPLOCDDTEYPVPVYQPAI 960
DB 901 TRWLLQELVLFLLWSVWGSWYDRGAESVFFHSHKHKKODPLOCDDTEYPVPVYQPAI 960
QY 961 REANGIVECCPCQKVFFVQIQIPNSNLLLVTDPTCDCSIIPPVLQEAATEVKYNASVKCDR 1020
DB 961 REANGIVECCPCQKVFFVQIQIPNSNLLLVTDPTCDCSIIPPVLQEAATEVKYNASVKCDR 1020
QY 1021 MRSQKLRRRPPDSCHAFHPEVRVREADRWAGFSSPNPLCLGLCPCRBQSHIGMPNTPVPVL 1080
DB 1021 MRSQKLRRRPPDSCHAFHPEVRVREADRWAGFSSPNPLCLGLCPCRBQSHIGMPNTPVPVL 1080
QY 1081 LGGNIRVYAL 1090
DB 1081 LGGNIRVYAL 1090
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RESULT 3

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US-10-128-558-176
; Sequence 176, Application US/10128558
; Publication No. US20040219521A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Gezhi
; APPLICANT: Boyle, Bryan J
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: 812A
; CURRENT APPLICATION NUMBER: US/10/128,558
; CURRENT FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: US 60/339,453
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: Pt_FL_genes Version 6.0
; SEQ ID NO 176
; LENGTH: 1207
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-128-558-176
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Query Match 94.1%; Score 5385.5; DB 16; Length 1207;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 1032; Conservative 6; Mismatches 13; Indels 3; Gaps 2;

QY 11 DRVKLWADTGGDLNTVTYKSGSLLOKVKYKDVESLSKTEEVDDGLELVRKFSSEDMENML 70
DB 145 ETVKLWADTGGDLNTVTYKSGSLLOKVKYKDVESLSKTEEVDDGLELVRKFSSEDMENML 204
```

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QY 71 RRKVEAVQNLVEAAEADLANHEFNESLVDYDYNVSLINERDEKGNFVELGAELLESNAH 130
DB 205 RRKVEAVQNLVEAAEADLANHEFNESLVDYDYNVSLINERDEKGNFVELGAELLESNAH 264
QY 131 FSNLPNTSISVOLPTNPNYKDPDILNGVYMSSEALNAVVENFORDPTLTWQYFGSATG 190
DB 265 FSNLPNTSISVOLPTNPNYKDPDILNGVYMSSEALNAVVENFORDPTLTWQYFGSATG 324
QY 191 FFRYIPGIKWTPDENGVIITFDCNRNGWYIOAATS PKD I V I L V D V S G S M K G L R M T I A K H T I 250
DB 325 FFRYIPGIKWTPDENGVIITFDCNRNGWYIOAATS PKD I V I L V D V S G S M K G L R M T I A K H T I 384
QY 251 TTILDTLGENDFNIIAYNDYVHYI BPCFKGILVQADRDNRHFKLLVBEELMKVGVGVD 310
DB 385 TTILDTLGENDFNIIAYNDYVHYI BPCFKGILVQADRDNRHFKLLVBEELMKVGVGVD 444
QY 311 QALREAFQILKQFEAKQKSLCNQAI ML I S D G A V E D Y E P F E K Y N W P D C K V R V T Y L I G R 370
DB 445 QALREAFQILKQFEAKQKSLCNQAI ML I S D G A V E D Y E P F E K Y N W P D C K V R V T Y L I G R 504
QY 371 EVSFADRMKWIACNNKGYTQI STLADTQENVNMEYLHVL SRPMVINHDHDI I M T E A Y M D S 430
DB 505 EVSFADRMKWIACNNKGYTQI STLADTQENVNMEYLHVL SRPMVINHDHDI I M T E A Y M D S 564
QY 431 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSVALRELKMLAPRYKLGVHG 490
DB 565 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSVALRELKMLAPRYKLGVHG 624
QY 491 AFLNTNNGYILSHPDRLPLYREGKCLKPKPNYSVDLSEVEDQAESLRTAMINRETGT 550
DB 625 AFLNTNNGYILSHPDRLPLYREGKCLKPKPNYSVDLSEVEDQAESLRTAMINRETGT 684
QY 551 LSMDVKVPMDKGRVLF LTNDYF FTDI S D T P F S L G A V L S R G H G E Y I L L G N T S V E E G L H D L 610
DB 685 LSMDVKVPMDKGRVLF LTNDYF FTDI S D T P F S L G V V L S R G H G E Y I L L G N T S V E E G L H D L 744
QY 611 LHPDLALAGDWIYCIITDIPDHRKLSOLEAMIRFLTRKDPDLSCDEBELVREVLFDVAVTA 670
DB 745 LHPDLALAGDWIYCIITDIPDHRKLSOLEAMIRFLTRKDPDLSCDEBELVREVLFDVAVTA 804
QY 671 PMEAYTALALANMSESEHVVDMAF LGTRAGLRLSSLFVGSEKVS DRKFLTPPEDEASVFT 730
DB 805 PMEAYTALALANMSESEHVVDMAF LGTRAGLRLSSLFVGSEKVS DRKFLTPPEDEASVFT 864
QY 731 LDRFPLWYRQASEHPAGSFVFNLRWAE GPESAGEPMVVTASTAVATVDKRTAIAAAGV 790
DB 865 LDRFPLWYRQASEHPAGSFVFNLRWAE GPESAGEPMVVTASTAVATVDKRTAIAAAGV 924
QY 791 QMKLEFLQRKFWAATRCQSTVDGPTQSCEDSDLD C F V I D N N G F I L I S K S R E T G R F L G E 850
DB 925 QMKLEFLQRKFWAATRCQSTVDGPTQSCEDSDLD C F V I D N N G F I L I S K S R E T G R F L G E 984
QY 851 VDGAVLTQLLSMGVFSQVTWYDYQAMCKPSSHHSAQAQPLVSPISAFLTATRWLLQELVL 910
DB 985 VDGAVLTQLLSMGVFSQVTWYDYQAMCKPSSHHSAQAQPLVSPISAFLTATRWLLQELVL 1044
QY 911 FLLEWSVWGSWYDRGAESVFFHSHKHKKQDPLQPCDTEYPVPVYQPAIREANGIVECG 970
DB 1045 FLLEWSVWGSWYDRGAESVFFHSHKHKKQDPLQPCDTEYPVPVYQPAIREANGIVECG 1104
QY 971 PCOKVFWVQIQIPNSNLLLVTDPTCDCSIIPPVLQEAATEVKYNASVKCDRMRSQKLRRP 1030
DB 1105 PCOKVFWVQIQIPNSNLLLVTDPTCDCSIIPPVLQEAATEVKYNASVKCDRMRSQKLRRP 1164
QY 1031 DSCHAFHPEVRVREADRWAGFSSPNP--LCLGLC 1062
DB 1165 DSCHAFHPEVRVREADRWAGFSSPNP--LCLGLC 1197
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RESULT 4

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US-10-257-174-34
; Sequence 34, Application US/10257174
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Qy	672	MEAYWTALALNMSESESHVVDMAFLGTRAGLLRSLFVGSBKVSDRKFLTTPDEASVFTL	733
Db	680	MEAYWTALALNMSESESHVVDMAFLGTRAGLLRSLFVGSBKVSDRKFLTTPDEASVFTL	739
Qy	732	DRPPLMYROASBHPAGSFVFNLRWARGESAGEPMVVTASTAVAVTVDKRTAIAAAAGVQ	791
Db	740	DRPPLMYROASBHPAGSFVFNLRWARGESAGEPMVVTASTAVAVTVDKRTAIAAAAGVQ	799
Qy	792	MKLEFLQRKFWAATRCQSTVDGPTQSCEDSDLDLDCFVIDNNGFILISKRSRETGRFLGEV	851
Db	800	MKLEFLQRKFWAATRCQSTVDGPTQSCEDSDLDLDCFVIDNNGFILISKRSRETGRFLGEV	859
Qy	852	DGAVLTQLLSMGVFSQVTWYDYQAMCKPSSHHSSAAQPLVSPISAFLTATRWLLQELVLF	911
Db	860	DGAVLTQLLSMGVFSQVTWYDYQAMCKPSSHHSSAAQPLVSPISAFLTATRWLLQELVLF	919
Qy	912	LLEWSVMGWSYDRGAEKSVFHHSHKKQDPLQPCDTEYFVYVYOPAIREANGIVECGP	971
Db	920	LLEWSVMGWSYDRGAEB-----HKHKKQDPLQPCDTEYFVYVYOPAIREANGIVECGP	972
Qy	972	CQKVFVWQIIPNSNLLLVTDPT-CDCSIFFPPVQEAETEVKYNASVKCDMRMSQKLRRP	1030
Db	973	CQKVFVWQIIPNSNLLLVTDPTFCRMGSGPEILTLTVASAHNASVKCDMRMSQKLRRP	1032
Qy	1031	DSCHAFHPBVRVEADRGWAGFSPPNP--LCILGLC	1062
Db	1033	DSCHAFHPBENAQ-DCGGASDTSASPPLLLLPVC	1065
RESULT 5			
US-10-257-174-35			
; Sequence 35, Application US/10257174			
; Publication NO. US20040034194A1			
; GENERAL INFORMATION:			
; APPLICANT: Agarwal, Pankaj			
; APPLICANT: Murgoch, Paul R.			
; APPLICANT: Rizvi, Safia K.			
; APPLICANT: Smith, Randall F.			
; APPLICANT: Xiang, Zhaoqing			
; TITLE OF INVENTION: NOVEL COMPOUNDS			
; FILE REFERENCE: GP50022			
; CURRENT APPLICATION NUMBER: US/10/257,174			
; CURRENT FILING DATE: 2002-10-10			
; PRIOR APPLICATION NUMBER: PCT/US01/11797			
; PRIOR FILING DATE: 2001-04-11			
; PRIOR APPLICATION NUMBER: 60/196,603			
; PRIOR FILING DATE: 2000-04-13			
; PRIOR APPLICATION NUMBER: 60/199,417			
; PRIOR FILING DATE: 2000-04-24			
; NUMBER OF SEQ ID NOS: 48			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 35			
; LENGTH: 1114			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-257-174-35			
Query Match			
Best Local Similarity 91.3%; Score 5230.5; DB 15; Length 1114;			
Matches 1010; Conservative 95.7%; Pred. No. 0;			
Matches 1010; Conservative 26; Indels 11; Gaps 4;			
Qy	11	DRVKLWDTFGDLYNTVTKYSGSLLLQKKYKOVESLKIIEVDGLVLRKFSDEMML	70
Db	58	ETVKLWDTFGDLYNTVTKYSGSLLLQKKYKOVESLKIIEVDGLVLRKFSDEMML	117
Qy	71	RRKVEAVQNLVEAAEADLNHEFNESLVFDYNSVLINERDEKGNFVELGAEPFLLENAH	130
Db	118	RRKVEAVQNLVEAAEADLNHEFNESLVFDYNSVLINERDEKGNFVELGAEPFLLENAH	177
Qy	131	FSNLPVNTSISVQLPTNVYKNDPDLNGVYMSALNAVVFENFQDPTLTWQYFGSATG	190
Db	178	FSNLPVNTSISVQLPTNVYKNDPDLNGVYMSALNAVVFENFQDPTLTWQYFGSATG	237


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Qy 191 FFRIYPGKWTDPDENGVLTFPCRNGWYIQAATSPKDIIVLVDSGSMKGLRMTIAKHTI 250
Db 238 FFRIYPGKWTDPDENGVLTFPCRNGWYIQAATSPKDIIVLVDSGSMKGLRMTIAKHTI 297
Qy 251 TTILDTLGENDFVNIIAVNDVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVD 310
Db 298 TTILDTLGENDFINIAYNDVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVD 357
Qy 311 QALREAFQILKQFQAKGSLCNAIMLISDGAVEDYEPPEKYNWDPCKVRVFTYILGR 370
Db 358 QALREAFQILKQFQAKGSLCNAIMLISDGAVEDYEPPEKYNWDPCKVRVFTYILGR 417
Qy 371 EVSFADRMKWTACNNKGYTTOISTLADTQENVMELHVLSPMVINHDHDIITEAYMDS 430
Db 418 EVSFADRMKWTACNNKGYTTOISTLADTQENVMELHVLSPMVINHDHDIITEAYMDS 477
Qy 431 KLLSSQAQSLTLLTTVAMPVFSKNETRSHGILLGVGSDVALRELKMLAPRYKLGHVGY 490
Db 478 KLLSSQAQSLTLLTTVAMPVFSKNETRSHGILLGVGSDVALRELKMLAPRYKLGHVGY 537
Qy 491 AFLTNNGYILSHPDRLPLVREGKLLPKPKPNYNSVDLSEVEWEDQASLSRTAMINRETGT 550
Db 538 AFLTNNGYILSHPDRLPLVREGKLLPKPKPNYNSVDLSEVEWEDQASLSRTAMINRETGT 597
Qy 551 LSMGVKVPMDKGRVLFETNDYFTDIDSPTPFLGAVLSRGHGYILLGNSTVEEGLHDL 610
Db 598 LSMGVKVPMDKGRVLFETNDYFTDIDSPTPFLGAVLSRGHGYILLGNSTVEEGLHDL 657
Qy 611 LHPDLALAGDWICYITDIDPHRKLSOLEAMIRFLTRKDPDCEDEELVREVLFDVVTA 670
Db 658 LHPDLALAGDWICYITDIDPHRKLSOLEAMIRFLTRKDPDCEDEELVREVLFDVVTA 717
Qy 671 PMEAYWTALALNMSESEHVVDMAFLGTRAGLLRSSLFVGVSEKYSDRKFLTPDEASVFT 730
Db 718 PMEAYWTALALNMSESEHVVDMAFLGTRAGLLRSSLFVGVSEKYSDRKFLTPDEASVFT 777
Qy 731 LDRPPLMYROASEHPAGSFVFNLRWAEPSGEPMPVMTASTAVAVTVDKRTAIAAAGV 790
Db 778 LDRPPLMYROASEHPAGSFVFNLRWAEPSGEPMPVMTASTAVAVTVDKRTAIAAAGV 837
Qy 791 QMKLEFLQRFWAATROCTVDBGYTQSCBDSLDLDCFVINDNNGFILLISKRSRETRFLGE 850
Db 838 QMKLEFLQRFWAATROCTVDBGYTQSCBDSLDLDCFVINDNNGFILLISKRSRETRFLGE 897
Qy 851 VDGAVLTQLLSMGVFSQVTWYDYQAMCKPSHHSSAAQPLVSPISAFELTATRWLLQLBLVL 910
Db 898 VDGAVLTQLLSMGVFSQVTWYDYQAMCKPSHHSSAAQPLVSPISAFELTATRWLLQLBLVL 957
Qy 911 FLLEWSVNGSWYDRGAESVFFHSHKHKKQDPLQPCDTEYPVFPYQPAIREANGIVECG 970
Db 958 FLLEWSVNGSWYDRGAESA-----HXHKQDPLQPCDTEYPVFPYQPAIREANGIVECG 1010
Qy 971 PCQKVFVVQIIPNSNLLLLVTDPDT-CDCSIPPPVLQATEVKYNASVKCDRMSRQKLRRR 1029
Db 1011 PCQKVFVVQIIPNSNLLLLVTDPDTFCRMGSGPEILLTITVASAHNASVKCDRMSRQKLRRR 1070
Qy 1030 PDSCHAPHEVRVREADRGWAGFSSPNP--LCLGLC 1062
Db 1071 PDSCHAPHEBNAQ-DCGGASDTSASPELLLLPVC 1104

```

RESULT 6

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US-10-257-022-12
; Sequence 12, Application US/10257022
; Publication No. US20030211499A1
; GENERAL INFORMATION:
; APPLICANT: REDDY, Roopa
; APPLICANT: THORNTON, Michael
; APPLICANT: BOWSKY, Mark L.
; APPLICANT: TANG, Y. Tom
; APPLICANT: KHAN, Farrah A.
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: GANDHI, Ameena R.

```

```

; APPLICANT: YAO, Monique G.
; APPLICANT: SANJANWALA, Madhusudan M.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: NGUYEN, Dannel B.
; APPLICANT: POLICKY, Jennifer L.
; APPLICANT: YUE, Henry
; APPLICANT: SEILHAMER, Jeffrey J.
; APPLICANT: WALIA, Narinder K.
; APPLICANT: LAL, Preeti
; APPLICANT: KEARNEY, Liam
; APPLICANT: WALSH, Roderick T.
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: LU, Yan
; APPLICANT: GREENE, Barrie D.
; APPLICANT: RAUMANN, Brigitte B.
; APPLICANT: Arvizu, Chandra S.
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: PI-0067 USN
; CURRENT APPLICATION NUMBER: US/10/257,022
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: US01/11206
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/195,595
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/196,872
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/199,020
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/200,552
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/202,348
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/203,495
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PERL Program
; SEQ ID NO 12
; LENGTH: 1310
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7473443CDI
US-10-257-022-12

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Query Match 66.5%; Score 3808; DB 15; Length 1310;
Best Local Similarity 80.5%; Pred. No. 4.3e-300;
Matches 750; Conservative 4; Mismatches 14; Indels 164; Gaps 2;

Qy 11 DRVKLWADTFGGDLVNTVTYKSGSLLLQKKYKDVESLSKIEEVDGLVLRKFSDEMMNL 70
Db 374 ETVKLWADTFGGDLVNTVTYKSGSLLLQKKYKDVESLSKIEEVDGLVLRKFSDEMMNL 433
Qy 71 RRKVEAVQNLVEAAAEADLNHFENSLV----- 98
Db 434 RRKVEAVQNLVEAAAEADLNHFENSLVBPFGVGVGMSVTQSGVGVGMSVTQSGVGV 493
Qy 99 ----- 98
Db 494 GVGMSITLSGVGVGMSVRSQSGVGVGMSVTQSGVGVGMSVTQSGVGVGMSVRSQ 553
Qy 99 ----- 98
Db 554 SGVGVGMSVTQSGWGFSAQRAAGACVDSGCRPAPALSSSHLRFRPSSLSACPGARAA 613
Qy 99 -----FDYNSVLINERDEKGNFVELGAEFLLESNAHPSNLPVNTSISVQLPTNV 149
Db 614 SVGLTRPPQFDYNSVLINERDEKGNFVELGAEFLLESNAHPSNLPVNTSISVQLPTNV 673
Qy 150 YNKDPDILNGVYMSEALNAVFVENFORDPTLTWQYFGSATGFFRIYPGKWTDPDENGVI 209
Db 674 YNKDPDILNGVYMSEALNAVFVENFORDPTLTWQYFGSATGFFRIYPGKWTDPDENGVI 733

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APPLICANT: Gu, Wei		1029	RPDSCHAFHPEVRVADRGWAGFSS	1053
TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS		1028	CGPCQKVFVVQOIPNSNLLLVTDPTCDSCSIFFPVLQEADEVKYNASVKCDRMSOKLRR	1028
FILE REFERENCE: 10448-190001		1027	CEDCSKSFVIOQIPSSNLFMVVVDSCSCLCSVAPITMAPIEIRYNESLKCERLKAQKIRR	1050
CURRENT APPLICATION NUMBER: US/10/162,012		1026	RPESCHGFHEE---ENARECGGASS	1072
PRIOR FILING DATE: 2002-06-04		1025	US-10-162-102-18	
PRIOR FILING DATE: 2000-06-06		1024	Sequence 18, Application US/10162102	
PRIOR APPLICATION NUMBER: US 09/875,321		1023	Publication No. US2003023236A1	
PRIOR FILING DATE: 2001-06-06		1022	GENERAL INFORMATION:	
PRIOR APPLICATION NUMBER: PCT/US01/18340		1021	APPLICANT: Curtis, Rory A.J.	
PRIOR FILING DATE: 2001-06-06		1020	APPLICANT: Silos-Santiago, Immaculada	
PRIOR APPLICATION NUMBER: US 60/209,257		1019	APPLICANT: Gu, Wei	
PRIOR FILING DATE: 2000-06-05		1018	TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS	
PRIOR APPLICATION NUMBER: US 09/875,423		1017	FILE REFERENCE: 10448-190001	
PRIOR FILING DATE: 2001-06-05		1016	CURRENT APPLICATION NUMBER: US/10/162,102	
PRIOR APPLICATION NUMBER: PCT/US01/18398		1015	CURRENT FILING DATE: 2003-04-04	
PRIOR FILING DATE: 2001-06-05		1014	PRIOR APPLICATION NUMBER: US 60/209,845	
PRIOR APPLICATION NUMBER: US 60/209,238		1013	PRIOR FILING DATE: 2000-06-06	
PRIOR FILING DATE: 2000-06-05		1012	PRIOR APPLICATION NUMBER: US 09/875,321	
PRIOR APPLICATION NUMBER: US 09/875,363		1011	PRIOR FILING DATE: 2001-06-06	
PRIOR FILING DATE: 2001-06-05		1010		
PRIOR APPLICATION NUMBER: PCT/US01/18247		1009		
PRIOR FILING DATE: 2001-06-05		1008		
PRIOR APPLICATION NUMBER: US 60/227,068		1007		
PRIOR FILING DATE: 2000-08-22		1006		
PRIOR APPLICATION NUMBER: US 09/928,530		1005		
PRIOR FILING DATE: 2001-08-13		1004		
PRIOR APPLICATION NUMBER: PCT/US01/25475		1003		
PRIOR FILING DATE: 2001-08-15		1002		
PRIOR APPLICATION NUMBER: US 60/226,770		1001		
PRIOR FILING DATE: 2000-08-21		1000		
PRIOR APPLICATION NUMBER: US 09/934,421		999		
PRIOR FILING DATE: 2001-08-21		998		
PRIOR APPLICATION NUMBER: PCT/US01/26096		997		
PRIOR FILING DATE: 2001-08-21		996		
PRIOR APPLICATION NUMBER: US 60/279,281		995		
PRIOR FILING DATE: 2001-03-28		994		
PRIOR APPLICATION NUMBER: US 10/109,029		993		
PRIOR FILING DATE: 2002-03-28		992		
PRIOR APPLICATION NUMBER: PCT/US02/09728		991		
PRIOR FILING DATE: 2002-03-28		990		
PRIOR APPLICATION NUMBER: US 60/290,288		989		
PRIOR FILING DATE: 2001-05-11		988		
PRIOR APPLICATION NUMBER: US (not assigned)		987		
PRIOR FILING DATE: 2002-05-13		986		
NUMBER OF SEQ ID NOS: 48		985		
SOFTWARE: FastSeq for Windows Version 4.0		984		
SEQ ID NO 18		983		
LENGTH: 1091		982		
TYPE: PRT		981		
ORGANISM: Mus musculus		980		
US-10-162-012-18		979		
Query Match		978		
Best Local Similarity		977		
Matches 627; Conservative 188; Mismatches 212; Indels 18; Gaps 6;		976		
13 VKLWADTFGGDLYNTVTKYSGSLLOKKYKDVESSLKIEEVDGLVLRKPSDEMMLRR		975		
42 VKLWASAFGGEIKIAKYSGSLLQKKYKEYEKDVAIEIDGLQVLKLAKEENEFHK		974		
73 KVEAVQNLVEAAEADLNHEFNESLVFDYNSVLINERDEKGNFVELGASFLLLESNAHFS		973		
102 KSEAVRLVEAAEAEHLKHEFDADLQVEYFNAVLINERDKDGNFLELGKSPILAPNDHFN		972		
133 NLPNTSISSVOLTNTYNDKPDILNGVYHSEALNAVVENFQDPDLTWQYFGSATGFF		971		
162 NLPNLSLSDVQVFTNTYNDKPDILNGVYHSEALNAVVENFQDPDLTWQYFGSATGFF		970		
193 RIYGIKWTDPENGVIATDCNRCRWYQAAATSPKDIIVLVDVSGSMKGLRTIAKHTITT		969		
222 RQYGIKWTDPENGVIATDCNRCRWYQAAATSPKDIIVLVDVSGSMKGLRTIAKHTITT		968		

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; PRIOR APPLICATION NUMBER: PCT/US01/18340
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,423
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18398
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,238
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,363
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18247
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/227,068
; PRIOR FILING DATE: 2000-08-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 1091
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-162-102-18

Query Match          59.8%; Score 3422; DB 15; Length 1091;
Best Local Similarity 60.0%; Pred. No. 8,7e-269;
Matches 627; Conservative 188; Mismatches 212; Indels 18; Gaps 6;

Qy 13 VKLWADTFGGDLVNTVTKYSGSLLQLKKYKXDVSSLLKIEVDGLVLRKFSDEMNNLRR 72
Db      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 42 VKLWASAFGGEIKSIAAKYSGSLLQLKKYKXDVSSLLKIEVDGLVLRKFSDEMNNLRR 101
Db      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 73 KVEAVONLVAAEEADLNHFEWNSLVFYDYNVSVLNERDEKGNFVGLGAEFLLESNAHFS 132
Db      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 102 KSEAVRRLVEAAEEAHLKHEFDADLQYEFYFNAVLINERDKGNFLEGLKEFILAPNDHFN 161
Db      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 133 NLPVNTSISSVOLPTNVYNNKDPDILNGVYMSALNAVVENFORDPTLTWQYFGSATGFF 192
Db      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 162 NLPVNTSISSVOLPTNVYNNKDPDILNGVYMSALNAVVENFORDPTLTWQYFGSATGFF 221
Db      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 193 RIYPGKWTDPDENGVTTFDCRNRGWYIOAATSPKDIIVLVDSGSMKGLRMTIAKHTITT 252
Db      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 222 RQYPGIKWEPDENGVIATFDCRNKRWYIOAATSPKDVILVDSGSMKGLRLTIKQTVSS 281
Db      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 253 ILDTLGENDFVNIAYNDVYHYTEPCFKGILVQADRDNRHFKLLVEELMVKGVVQDOA 312
Db      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 282 ILDTLGDGDDFFNIITNEELHYVEPCNLGTLVQADRTNKEHFRHLDKJFAKGIGMLDIA 341
Db      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 313 LREAFQILKQFBAKQGSCLNQAIMLISDGAVEDYBPVFEKYNWPCVKRVFTYLIIGREV 372
Db      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 342 LNEAFNLSDFNHTGGGSCSQAIMLITDGAVDYDTIFAKYNWPKRVIFTYLIIGREA 401
Db      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 373 SPADRMKWIACNNKGYTQISTLADQENNVMEYHLVSRPMVINHDHDIITWYAYWDSKL 432
Db      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 402 AFADNLKMWACANKGFQISTLADQENNVMEYHLVSRPMVINHDHDIITWYAYWDSKL 461
Db      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 433 LSSQA---QSLTLLTTVAMPVSKNETSHGILLGWGSDVALBELMKLAPRYKLGVH 488
Db      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 462 PQAKLADDGGLVMTTAMPVSKNETSKGILLGWGSDVALBELMKLAPRYKLGVH 521
Db      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 489 GYAFLNTNNGYIILSHPDRLRYREGKKLKPKNYNSVDLSEWEDQABSLRTAMINRET 548
Db      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 522 GYAFAITNNGYIILTHPELRPLYEGKK-REKPNYSSVDLSEWEDQABSLRTAMINRET 580
Db      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 549 GTLSMDVKVPMWKGKRVLFTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVBEGLH 608
Db      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 581 GKFSEMEYKTVDKGKRVLWNTNDYYTDDIKGTFPSLGLVALSRGHGKYFPRGNVTIEGLH 640
Db      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 609 DLLHPPDLALAGDWICYITDDPHRKLISOLEAMIRFLTRKDPDLECDDEELVREVLDAVV 668
Db      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 641 DLEHPPDVSLADEWSYCNNTDULHPSHRHLSQLEAKLYLKGEPLQCDKELIQEVLDAVV 700
Db      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCE: 180
; CURRENT APPLICATION NUMBER: US/10/902,531
; CURRENT FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: US/09/397,550
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 1077
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-902-531-24

Query Match          59.7%; Score 3419.5; DB 17; Length 1077;
Best Local Similarity 60.3%; Pred. No. 1.4e-268;
Matches 622; Conservative 188; Mismatches 206; Indels 15; Gaps 5;

Qy 13 VKLWADTFGGDLVNTVTKYSGSLLQLKKYKXDVSSLLKIEVDGLVLRKFSDEMNNLRR 72
Db      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 42 VKLWASAFGGEIKSIAAKYSGSLLQLKKYKXDVSSLLKIEVDGLVLRKFSDEMNNLRR 101
Db      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 73 KVEAVONLVAAEEADLNHFEWNSLVFYDYNVSVLNERDEKGNFVGLGAEFLLESNAHFS 132
Db      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 102 KSEAVRRLVEAAEEAHLKHEFDADLQYEFYFNAVLINERDKGNFLEGLKEFILAPNDHFN 161
Db      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 133 NLPVNTSISSVOLPTNVYNNKDPDILNGVYMSALNAVVENFORDPTLTWQYFGSATGFF 192
Db      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 162 NLPVNTSISSVOLPTNVYNNKDPDILNGVYMSALNAVVENFORDPTLTWQYFGSATGFF 221
Db      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 193 RIYPGKWTDPDENGVTTFDCRNRGWYIOAATSPKDIIVLVDSGSMKGLRMTIAKHTITT 252
Db      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 222 RQYPGIKWEPDENGVIATFDCRNKRWYIOAATSPKDVILVDSGSMKGLRLTIKQTVSS 281
Db      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 253 ILDTLGENDFVNIAYNDVYHYTEPCFKGILVQADRDNRHFKLLVEELMVKGVVQDOA 312
Db      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

; SEQUENCE 24, Application US/10902531
; Publication No. US20050042659A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCE: 180
; CURRENT APPLICATION NUMBER: US/10/902,531
; CURRENT FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: US/09/397,550
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 1077
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-902-531-24
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; Sequence 15, Application US/10162102		Db	462	--POAQLTDDQGPVLMTTVAMPVFSKQNETRSKIGILLGVVGTDPVPVKELLKTIPKYLK	519
; Publication No. US20030232336A1		Qy	487	VHGAFALNTNNGYILSHPDRLRPLYREGKLLKPKPNYSVDLSEVWEDQAESELTAMNR	546
; GENERAL INFORMATION:		Db	520	IHGAFALNTNNGYILTHPELRLLYEKGK-RRKPNYSVDLSEVWEDRDDVLRNMMVR	578
; APPLICANT: Curtiss, Rory A.J.		Qy	547	ETGLTSDVQVPMKGRVLFLTNDYFFTDISDTPPSLGAIVLSRGHGEYILLGNSTVEEG	606
; APPLICANT: Silos-Santiago, Inmaculada		Db	579	KTGKFSMEVKTVDKGRVLMTNDYYTIDIKGTPPSLGVALSRGHGKIFYFRGNVTITEEG	638
; APPLICANT: Gu, Wei		Qy	607	LHDLHPDLALAGDWIYCIITDIDPHRKLQLEAMIRFLTRKDPDLCEBELREVLFDA	666
; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS		Db	639	LHDLHPDVSILADEWSYCNTDLHPEHRHLSQLEAIKLYLKGKPELLOCDKELIQEVLFDA	698
; FILE REFERENCE: 10448-190001		Qy	667	VVTAPMEAYMTALALNNSESEHVVDMAFLGTRAGLLRSLFVSGSEKVSORKKFLTTPDEA	726
; CURRENT APPLICATION NUMBER: US/10/162,102		Db	699	VVSAPTEAYMTSLALNKSSENSDKGVEVAFGLTRTGLSRINLFLVGAELTNQDFLKGADKE	758
; PRIOR FILING DATE: 2003-04-04		Qy	727	SVETLDRFPLWYRQASEHPAGSFVNLRWAEGPSAGEPMVVTASTAVATVTKRTAIAA	786
; PRIOR FILING DATE: 2000-06-06		Db	759	NIFNADHFFLWYRRAAEQIPGSFVYSIPFSTGP--VNKSNVVTASTSIQLLDERKSPVA	816
; PRIOR APPLICATION NUMBER: US 60/209,845		Qy	787	AAGVQMKLEFLQKFWAATRCQCTVDGPTYQSCEDSDLDCCFVIDNNGFILISKRSTGR	846
; PRIOR FILING DATE: 2001-06-05		Db	817	AVGIQMKLEFFQKFWTASQCASLDGKCSISCDDETVCYLIDNNGFILVSEDTQTGD	876
; PRIOR APPLICATION NUMBER: US 09/875,321		Qy	847	FLGEVDGAVLTQLLSMGVFSQVTMYQYQAMCKPSSHHSSAAQPLVSPISAPLATRMLLQ	906
; PRIOR FILING DATE: 2001-06-06		Db	877	FFGEIEGAVNMKLLTMGSKFRITLYDQAMCRANKESSDGAHGLLDPYNAPLSAVKIMT	936
; PRIOR APPLICATION NUMBER: US 60/209,257		Qy	907	ELVLFILENSVGSWYDRGAESVHHSHKHKKQDPLOPCDTEYFVYVQPAIREANGI	966
; PRIOR FILING DATE: 2000-06-05		Db	937	ELVLFILENSVGSWYDRGAESVHHSHKHKKQDPLOPCDTEYFVYVQPAIREANGI	988
; PRIOR APPLICATION NUMBER: US 09/875,423		Qy	967	VECGPCQKVFVQOIPNSNLLLVLTPTCDCSIFPPVLQBEATEVKYNASVKCDRMRSQL	1026
; PRIOR FILING DATE: 2001-06-05		Db	989	IACEDCSKSFVIOQIPSSNLFMVVVDSSCLCESVAPITMAPIEIRYNESLKCELRKAKI	1048
; PRIOR APPLICATION NUMBER: PCT/US01/18398		Qy	1027	RRRPDSCHAFPE	1039
; PRIOR FILING DATE: 2001-06-05		Db	1049	RRRPDSCHAFPE	1061
; PRIOR APPLICATION NUMBER: US 60/209,238		RESULT 14			
; PRIOR FILING DATE: 2000-06-05		US-10-924-081-6			
; PRIOR APPLICATION NUMBER: US 09/875,363		; Sequence 6, Application US/10924081			
; PRIOR FILING DATE: 2001-06-05		; Publication No. US20050095678A1			
; PRIOR APPLICATION NUMBER: US 60/209,068		; GENERAL INFORMATION:			
; PRIOR FILING DATE: 2000-08-22		; APPLICANT: PARKER, David			
; Remaining Prior Application data removed - See File Wrapper or PALM.		; APPLICANT: XU, Xianghong			
; NUMBER OF SEQ ID NOS: 48		; APPLICANT: KHAWAJA, Afshen			
; SOFTWARE: FastSeq for Windows Version 4.0		; TITLE OF INVENTION: NOVEL RAT CALCIUM CHANNEL SUBUNITS AND			
; SEQ ID NO 15		; TITLE OF INVENTION: RELATED PROBES, CELL LINES AND METHODS			
; LENGTH: 1091		; FILE REFERENCE: 381092001400			
; ORGANISM: Homo sapiens		; CURRENT APPLICATION NUMBER: US/10/924,081			
US-10-162-102-15		; PRIOR FILING DATE: 2004-08-23			
Query Match 59.7%; Score 3416.5; DB 15; Length 1091;		; PRIOR FILING DATE: 2004-08-23			
Best Local Similarity 60.3%; Pred. No. 2,4e-268;		; PRIOR APPLICATION NUMBER: PCT/CA2004/001550			
Matches 623; Conservative 188; Mismatches 203; Indels 19; Gaps 6;		; PRIOR FILING DATE: 2004-08-23			
Qy 13 VKLWADTFGDLVNTVTKYSGSLLLQKXYKDVESLKIIEVDGLLELVKFSSEDMENMLRR		; PRIOR APPLICATION NUMBER: US 60/497,096			
Db 42 VKLWASAFGGEIKSIAAKYSGSLLLQKXYKDVESLKIIEVDGLLELVKFSSEDMENMLRR		; NUMBER OF SEQ ID NOS: 22			
Qy 73 KVEAVQNLVRAAEADLNHEFNESLVFDYNSVLINERDEKGNFVELGASFLLESNAHPS		; SOFTWARE: FastSeq for Windows Version 4.0			
Db 102 KSEAVRLVRAAEAEHUKHBFADLQYEFYNAVILINERDKGNFLEUGKGFILAPNDHFN		; SEQ ID NO 6			
Qy 133 NLPVNTSISVQLPTVNTYKDPDILNGVYMSALNAVVENFQRPDPTLTWQYFGSATGFF		; LENGTH: 1091			
Db 162 NLPVNTSISVQLPTVNTYKDPDILNGVYMSALNAVVENFQRPDPTLTWQYFGSATGFF		; TYPE: PRT			
Qy 193 RIYPGIKWTPDENGVIITFCRNRGWYIQAATSPKDVILVDVSGSMKGLMTAKHTITT		; ORGANISM: Rattus norvegicus			
Db 222 RQYPGIKWTPDENGVIITFCRNRGWYIQAATSPKDVILVDVSGSMKGLMTAKHTITT		US-10-924-081-6			
Qy 253 ILDTLGENDFWIIITAYNDYHYIEPCFKGILLVQADRNREHFKLLVEELMVKGVVQDA		Query Match 59.6%; Score 3411; DB 17; Length 1091;			
Db 282 ILDTLGENDFWIIITAYNDYHYIEPCFKGILLVQADRNREHFKLLVEELMVKGVVQDA		Best Local Similarity 59.6%; Pred. No. 6.8e-268;			
Qy 313 LREAFQILKFOEAKQGLNCAIMLISDGAVEDYEPVFEKYNWPCDKVRVFTYLIQREV		Matches 623; Conservative 191; Mismatches 213; Indels 18; Gaps 6;			
Db 342 LNEAFNLSDFNHTGQSSCAIMLITDGAVDYDTIFAKYNWPCDKVRVFTYLIQREV					
Qy 373 SFADRMKVIACNKGYYTQISTLADTQENWYELHVLSPRWVINHDHDIITWTEAYMDSKL					
Db 402 AFADNLKWMACANKGFTQISTLADTQENWYELHVLSPRWVINHDHDIITWTEAYMDSKL					
Qy 433 LSSQAQSLT-----LLTVMVPVFSKNETRSKIGILLGVVGTDPVPVKELLKTIPKYLK					

Qy 13 VKLWADTFGGDLVNTVTYKSGSLLOKKYKDVESLSKIEEVDGLVLRKFSDEMMLRR 72
Db 42 VKLWASAFGGEIKSIAAKYSGSLLQKKYKEYEKDVAIEIDGLQLVKLAKWNEEMPHK 101
Qy 73 KVEAVQNLVEAAEADLNHEFNESLVDYVNSVLINERDEKGNFVGLGAEFLLESNAHFS 132
Db 102 KSEAVRRLVEAAEBAHLKHEFDADLOQYEFNAVLINERDKGNFLELGKEFILAPNDHFN 161
Qy 133 NLPVNTSISVOLPTNVYNKDPDILNGVYMSALNAVVENFORDPDLTWQYFGSAGTFF 192
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Qy 193 RIYPGKIWTPDENGVIITFCRNRGWYIQAATSPKDIIVLVDVSGSMKGLRMTAKHTITT 252
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Qy 373 SFADRMKWIACNNKGYITQISTLADTQENMEYLHLVLSRPMVINHDHDIITWEAYMDSKL 432
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; Sequence 12, Application US/10902531
; Publication No. US20050042659A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCES: 180
; CURRENT APPLICATION NUMBER: US/10/902,531
; CURRENT FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: US/09/397,550
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 1065
; TYPE: PRP
; ORGANISM: Homo sapiens
US-10-902-531-12

Query Match 59.6%; Score 3410.5; DB 17; Length 1065;
Best Local Similarity 60.3%; Pred. No. 7.2e-268;
Matches 619; Conservative 188; Mismatches 207; Indels 13; Gaps 5;
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Search completed: November 16, 2005, 03:37:42
Job time : 180 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 17, 2005, 03:21:06 ; Search time 1916 Seconds
(without alignments)
4704.647 Million cell updates/sec

Title: US-09-833-222A-10
Perfect score: 5726
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9794790 seqs, 4134909567 residues

Total number of hits satisfying chosen parameters: 19589580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
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Database : Published Applications NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	5726	100.0	3486	17	US-10-119-624-9
3	5385.5	94.1	4841	21	US-10-128-558-52
4	5234.5	91.4	3228	19	US-10-257-174-10
5	5230.5	91.3	3345	19	US-10-257-174-11
6	3808	66.5	4125	18	US-10-257-023-27
7	3422.5	59.8	3598	22	US-10-924-081-5
8	3421.5	59.8	3528	9	US-09-728-628-12
9	3421.5	59.8	3528	24	US-10-972-024-117
10	3416.5	59.7	3276	9	US-09-875-423-3
11	3416.5	59.7	3276	15	US-10-162-012-16
12	3416.5	59.7	3276	18	US-10-162-102-16
13	3416.5	59.7	3690	9	US-09-875-423-1
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17	3400.5	59.4	3213	22	US-10-902-531-9
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19	3278.5	57.3	3057	22	US-10-902-531-7
20	3195.5	55.8	3382	20	US-10-478-758-13
21	2944.5	51.4	3172	22	US-10-924-081-8
22	2306	40.3	1523	18	US-10-334-143-107
23	1792.5	31.3	1050	22	US-10-902-531-15
24	1695	29.6	969	22	US-10-902-531-14
25	1598	27.9	912	22	US-10-902-531-13
26	1410	24.6	6519	26	US-11-097-143-30665
27	1362.5	23.6	856	19	US-10-220-120-103
28	1336.5	23.3	3414	26	US-11-097-143-13493
29	1329	23.2	13293	26	US-11-097-143-30664
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31	1192	20.8	5733	21	US-10-417-375-171
32	1188.5	20.8	5279	15	US-10-116-949-5
33	1188	20.7	4993	22	US-10-924-081-2
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40	1184.5	20.7	3474	22	US-10-924-081-10
41	1182	20.6	5386	21	US-10-417-375-168
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45	1150.5	20.1	3186	22	US-10-902-531-1

ALIGNMENTS

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; Sequence 9, Application US/09833222A
; Publication No. US20030166045A1
; GENERAL INFORMATION:
; APPLICANT: Qin, Ning
; APPLICANT: Codd, Ellen
; TITLE OF INVENTION: cdna encoding the Calcium Channel Alpha2Delta-4 Subunit
; FILE REFERENCE: calcium channel alpha2delta-4 subunit
; CURRENT APPLICATION NUMBER: US/09/833,222A
; CURRENT FILING DATE: 2001-04-01
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-222A-9

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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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US-09-833-222A-10 (1-1090) x US-09-833-222A-9 (1-3486)

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Db 1510 ACACTGCTCACCACTGTGGCCATGTCAGTCTTTCAGCAAGAGAAACGAAACCGCATCCAT 1569
Qy 461 GlyIleLeuLeuGlyValValGlySerAspValAlaLeuArgGluLeuMetLysLeuAla 480
Db 1570 GGCATTCTCTGGGTGTGGTGGCTCAGATGTGGCCCTGAGAGAGTGTGAAGCTGGCG 1629
Qy 481 ProArgTyrLysLeuGlyValHisGlyTyrAlaPheLeuAsnThrAsnAsnGlyTyrIle 500
Db 1630 CCCCAGTACAAGCTTGGAGTGACGGATACGCTTTCTGAACACCAACCAATGGCTACATC 1689
Qy 501 LeuSerHisProAspLeuArgProLeuTyrArgGluGlyLysLysLeuLysProLysPro 520
Db 1690 CTCTCCATCCCGACCTCCGCCCCCTGTACAGAGAGGGAGAAACTAAAAACCAACCT 1749
Qy 521 AsnTyrAsnSerValAspLeuSerGluValGluTrpGluAspGlnAlaGluSerLeuArg 540
Db 1750 AACTACAACAGTGTGGATCTCTCCGAAGTGGAGTGGGAAGACCCAGGCTGAATCTCTGAGA 1809
Qy 541 ThrAlaMetIleAsnArgGluThrGlyThrLeuSerMetAspValLysValProMetAsp 560
Db 1810 ACAGCCATGATCAATAGGAAACAGGTACTCTCTCGATGGATGTGAAGGTTCGATGGAT 1869
Qy 561 LysGlyLysArgValLeuPheLeuThrAsnAspTyrPhePheThrAspIleSerAspThr 580
Db 1870 AAAGGAAAGCGAGTCTTTCTCTGACCAATGACTACTTCTTCACGGACATCAGCGACCC 1929
Qy 581 ProPheSerLeuGlyAlaValLeuSerArgGlyHisGlyGluTyrIleLeuLeuGlyAsn 600
Db 1930 CCTTTTCAGTTTGGGGCGGTGTCTCCCGGGCCACCGAGAATACATCTCTCTGGGGAAC 1989
Qy 601 ThrSerValGluGluGlyLeuHisAspLeuLeuHisProAspLeuAlaLeuAlaGlyAsp 620
Db 1990 AGCTGTGGAGAGAGGCTGATGACTTGTTCACCCAGACCTGGCCCTGGCGGTGAC 2049
Qy 621 TrpIleTyrCysIleThrAspIleAspProAspHisArgLysLeuSerGlnLeuGluAla 640
Db 2050 TGGATCTACTGCAATACAGATATTACCAGACCAACCGAAGCTCAGCCAGCTAGAGGCC 2109
Qy 641 MetIleArgPheLeuThrArgLysAspProAspLeuGluCysAspGluGluLeuValArg 660
Db 2110 ATGATCCGCTTCTCTACCGAGGAGGACCCAGACCTGGAGTGTGACGAGGAGCTGGTCCGG 2169
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Qy 661 GluValLeuPheAspAlaValValThrAlaProMetGluAlaTyrTrpThrAlaLeuAla 680
Db 2170 GAGGTGCTGTTGACGGGTGGTGGACAGCCCATGGAGCCCTACTGGACAGCGCTGGCC 2229
Qy 681 LeuAsnMetSerGluGlnSerGluHisValValAspMetAlaPheLeuGlyThrArgAla 700
Db 2230 CTCAACATGTCCGAGGAGTCTGAACACGTGTGGACATGGCCCTTCCTGGGCAACCGGGCT 2289
Qy 701 GlyLeuLeuArgSerSerLeuPheValGlySerGluLysValSerAspArgLysPheLeu 720
Db 2290 GGCTCTCTGAGAACGACCTTGTTCGTGGCTCCGAGAGGTCTCCGACAGAAAGTTCCTG 2349
Qy 721 ThrProGluAspGluAlaSerValPheThrLeuAspArgPheProLeuTyrPyrArgGln 740
Db 2350 ACACCTGAGGACGAGGCGAGCGTGTTCACCTGAGCCGCTTCGCGCTGTGTATCCGCGAG 2409
Qy 741 AlaSerGluHisProAlaGlySerPheValPheAsnLeuArgTrpAlaGluGlyProGlu 760
Db 2410 GCCTCAGAGCATCTGCTGGCAGCTTCGCTTCAACCTCCGCTGGGCGAGAGCACAGAA 2469
Qy 761 SerAlaGlyGluProMetValValThrAlaSerThrAlaValAlaValThrValAspLys 780
Db 2470 AGTGGGGTGAACCCATGGTGGTGGCGGAGCACAGCTGTGGCGTGGACCTGGGACAG 2529
Qy 781 ArgThrAlaIleAlaAlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLys 800
Db 2530 AGGACAGCCATTGCTGCAGCGCGGGCGTCCAAATGAAGCTGGAATTCCTCCAGCGCAA 2589
Qy 801 PheTrpAlaIleThrArgGlnCysSerThrValAspGlyProTyrThrGlnSerCysGlu 820
Db 2590 TTCTGGCGGCAACCGCGCAGTGCAGCACTGTGATGGGCGGTACACACAGAGCTGCGAG 2649
Qy 821 AspSerAspLeuAspCysPheValIleAspAsnGlyPheIleLeuIleSerLysArg 840
Db 2650 GACAGTGATCTGACTGCTTCGTCATCGAACACACGCGGTTCATTCGATCTCCAGAGG 2709
Qy 841 SerArgGluThrGlyArgPheLeuGlyGluValAspGlyAlaValLeuThrGlnLeuLeu 860
Db 2710 TCCCGAGAGACGGAGATTTCTGGGGAGGTGGTGTCTGTCTGACCCAGCTGCTC 2769
Qy 861 SerMetGlyValPheSerGlnValThrMetTyrAspTyrGlnAlaMetCysLysProSer 880
Db 2770 AGCATGGGGGTGTTACGCAAGTGAATGTATGACTATCAGGCCATGTGCAAAACCTCG 2829
Qy 881 SerHisHisSerAlaAlaGlnProLeuValSerProIleSerAlaPheLeuThrAla 900
Db 2830 AGTCACCAACACAGTGCAGCCAGCCCTGCTGTCAGCCCAATTTCTGCCTTCTTGACGGCG 2889
Qy 901 ThrArgTrpLeuLeuGlnGluLeuValLeuPheLeuLeuGluTrpSerValTrpGlySer 920
Db 2890 ACCAGGTGGCTGTCAGGAGCTGGTGTCTGCTGCTGAGTGGAGTGTCTGGGGCTCC 2949
Qy 921 TrpTyrAspArgGlyAlaGluAlaLysSerValPheHisHisSerHisLysLysLys 940
Db 2950 TGGTACACAGAGGGGCGAGGCCAAAGTGTCTTCATCACTCCCAACAAACAAGAAG 3009
Qy 941 GlnAspProLeuGlnProCysAspThrGluTyrProValPheValTyrGlnProAlaIle 960
Db 3010 CAGACCCGCTGCAGCCCTCGCACAGAGTACCCCGTGTCTGTTACAGCGCGGCATC 3069
Qy 961 ArgGluAlaAsnGlyIleValGluCysGlyProCysGlnLysValPheValValGlnGln 980
Db 3070 CGGAGGCCAACCGGATCGTGGAGTGGCGGCGCTGCCAGGAAGGTATTGTGGTGCAGCAG 3129
Qy 981 IleProAsnSerAsnLeuLeuLeuValThrAspProThrCysAspCysSerIlePhe 1000
Db 3130 ATTCCCAACAGTAACCTCTCTCTCTGTCAGACAGCCCACTGTGATCTCAGCATCTTC 3189
Qy 1001 ProProValLeuGlnGluAlaThrGluValLysTyrAsnAlaSerValLysCysAspArg 1020
Db 3190 CCACCACTGCTGAGGAGGCGACAGAGTCAATATATATGCTCTGTCAATGTGACCGG 3249
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Qy 1021 MetArgSerGlnLysLeuArgArgProAspSerCysHisAlaPheHisProGluVal 1040
Db 3250 ATGCGCTCCAGAAAGCTCCGCGCGACAGAGACTCTCTGCCACGCTTCCATCCAGAGGTG 3309
Qy 1041 ArgValGluAlaAspArgGlyTrpAlaGlyPheSerSerProAsnProLeuCysLeuGly 1060
Db 3310 CGGGTTGAGCGGATCGAGGGTGGGTGGAATTTTCATCCCAACCCCTCTGTGCTGGGT 3369
Qy 1061 LeuCysProCysArgGlnGluHisIleGlyMetProMetAsnThrProValProValLeu 1080
Db 3370 CTGTGCCCTGCAGACAGGAGCATATAGGGATGCCAATGAACACACCTGTGCTGTCTT 3429
Qy 1081 LeuGlyGlyAsnIleArgValTyrAlaLeu 1090
Db 3430 CTCGGGGAAACATTCCGGTTTATGCCCTG 3459

RESULT 2
US-10-119-624-9
; Sequence 9, Application US/10119624
; Publication No. US20030170785A1
; GENERAL INFORMATION:
; APPLICANT: Qin, Ning
; APPLICANT: Codd, Ellen
; TITLE OF INVENTION: cDNA Encoding a Human No. US20030170785A1el Alpha2 Delta4 Calcium
; FILE REFERENCE: ORT-1622
; CURRENT APPLICATION NUMBER: US/10/119,624
; CURRENT FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US 09/833,222
; PRIOR FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 3486
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-119-624-9

Alignment Scores:
Pred. No.: 0 Length: 3486
Score: 5726.00 Matches: 1090
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-833-222a-10 (1-1090) x US-10-119-624-9 (1-3486)
Qy 1 MetAlaValAlaLeuGlyThrArgArgAspArgValLysLeuTPAlaAspThrPhe 20
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Qy 21 GlyGlyAspLeuTyrAsnThrValThrLysTyrSerGlySerLeuLeuGlnLysLys 40
Db 250 GGGCGGGAGCTGTATAACACTGTGACCAATACTCAGGCTCTCTCTTGTGCGAAGAAG 309
Qy 41 TyrLysAspValGluSerSerLeuLysIleGluGluValAspGlyLeuGluLeuValArg 60
Db 310 TACAAGATGTGGAGTCCAGTCTGAAGATCGAGGAGTGGATGGCTTGGAGCTGGTGAGG 369
Qy 61 LysPheSerGluAspMetGluAsnMetLeuArgLysValGluAlaValGlnAsnLeu 80
Db 370 AAGTTCTCAGAGACATGGAGAACATGCTCGGAGGAAAGTCCGCGGCTCCAGAAATCTG 429
Qy 81 ValGluAlaAlaGluAlaAspLeuAsnHisGluPheAsnGluSerLeuLeuValPheAsp 100
Db 430 GTGGAAGCTGCCGAGGAGGCGGACCTGAACACGAATTCATGAATCCCTGGTTCGAC 489
Qy 101 TyrTyrAsnSerValLeuIleAsnGluArgAspGluLysGlyAsnPheValGluLeuGly 120
Db 490 TATTACAACCTCGTCTCTGATCAACAGAGAGGAGGAGCAACTTCGTGGAGCTGGGC 549
Qy 121 AlaGluPheLeuLeuGluSerAsnAlaHisPheSerAsnLeuProValAsnThrSerIle 140
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Db 550 GCCGAGTTCCTCGGAGTCCAATGCTCACTTCAGCAACCTGCGCGTGAACACCTCCATC 609
Qy 141 SerSerValGlnLeuProThrAsnValTyrAsnLysAspProAspIleLeuAsnGlyVal 160
Db 610 AGCAGCGTGAGCTGCCCAACGCTGTACAACAAAGACCCAGATATTTTAAATGGAGTC 669
Qy 161 TyrMetSerGluAlaLeuAsnAlaValPheValGluAsnPheGlnArgAspProThrLeu 180
Db 670 TACATGTCGAGCCCTGAATGCTGCTTCGTGGAGNACTTCAGAGAGACCCACAGCTTG 729
Qy 181 ThrTrpGlnTyrPheGlySerAlaThrGlyPhePheArgIleTyrProGlyIleLysTrp 200
Db 730 ACCTGGCAATATTTTGGCAGTGCAACTGGATTTCTCAGGATCTATCCAGGTATATAAATGG 789
Qy 201 ThrProAspGluAsnGlyValIleThrPheAspCysArgAsnArgGlyTyrTyrIleGln 220
Db 790 ACACCTGATGAGAAATGGATGCTTACTTTTGTGACCTGCCGAACCGCGCTGGTACATTCAA 849
Qy 221 AlaAlaThrSerProLysAspIleValIleLeuValAspValSerGlySerMetLysGly 240
Db 850 GCTGCTACTTCTCCCAAGGACATAGTATTTTGTGGACGTGAGCGCAGTATGAAGGGG 909
Qy 241 LeuArgMetThrIleAlaLysHisThrIleThrThrIleLeuAspThrLeuGlyGluAsn 260
Db 910 CTGAGGATGACTATTGCAAGCACACCATCACCACCATCTTGGACACCCCTGGGGGAGAT 969
Qy 261 AspPheValAsnIleIleAlaTyrAsnAspTyrValHisTyrIleGluProCysPheLys 280
Db 970 GACTTCGTTAAATCATAGCGTACAATGACTAGCTCCATTACATCAGAGCCCTGTTTAA 1029
Qy 281 GlyIleLeuValGlnAlaAspArgAspAsnArgGluHisPheLysLeuLeuValGluGlu 300
Db 1030 GGGATCTCTGCCAGCGGACCGAGACATTCGAGAGCATTTCAAACCTGCTGGTGGAGGAG 1089
Qy 301 LeuMetValLysGlyValGlyValValAspGlnAlaLeuArgGluAlaPheGlnIleLeu 320
Db 1090 TTGATGGTCAAAGGTGTGGGGGTGCTGGACCAAGCCCTCGAGAAAGCCCTTCAGATCCTG 1149
Qy 321 LysGlnPheGlnGluAlaLysGlnGlySerLeuCysAsnGlnAlaIleMetLeuIleSer 340
Db 1150 AAGCAGTTCCAGAGGCCAAGCAAGGAAGCCCTCGCAACCGAGCCCATCATGCTCATCAGC 1209
Qy 341 AspGlyAlaValGluAspTyrGluProValPheGluLysTyrAsnTrpProAspCysLys 360
Db 1210 GACGGCGCGTGGAGGACTACGAGCGGTGTTTGGAGAGTATAACTGGCCAGACTCTAAG 1269
Qy 361 ValArgValPheThrTyrIleuIleGlyArgGluValSerPheAlaAspArgMetLysTrp 380
Db 1270 GTCCGAGTTTTCATTACCTCAVTGGGAGAGAGTGTCTTTTGTGACCGCATGAAGTGG 1329
Qy 381 IleAlaCysAsnAsnLysGlyTyrTyrThrGlnIleSerThrLeuAlaAspThrGlnGlu 400
Db 1330 ATTGCGATGCACAAACAAAGGCTACTACGCGATCTCAACGCTGGCGGACACCCAGGAG 1389
Qy 401 AsnValMetGluTyrLeuHisValLeuSerArgProMetValIleAsnHisAspHisAsp 420
Db 1390 AACGTGATGGAAATACCTGCACGCTGCTCAGCGGCCCTGCTCATCAACCAAGCACGAC 1449
Qy 421 IleIleTrpThrGluAlaTyrMetAspSerLysLeuLeuSerSerGlnAlaGlnSerLeu 440
Db 1450 ATCATCTGGACAGAGGCCCTACATGGGACAGCAAGCTCTCAGCTCGCAGGCTCAGAGCCTG 1509
Qy 441 ThrLeuLeuThrThrValAlaMetProValPheSerLysLysAsnGluThrArgSerHis 460
Db 1510 ACACCTGCTACCCACTGTGGCCATGCCAGTCTTCAGCAAGNACCGAAACCGCATCCCCAT 1569
Qy 461 GlyIleLeuLeuGlyValValGlySerAspValAlaLeuArgGluLeuMetLysLeuAla 480
Db 1570 GGCATTTCTCTGGGTGTGGTGGCTCAGATGTGGCCCTCAGAGAGCTGATGAAGCTGGCG 1629
Qy 481 ProArgTyrLysLeuGlyValHisGlyTyrAlaPheLeuAsnThrAsnAsnGlyTyrIle 500
Db 1630 CCCCAGTACAAGCTTGGAGTGCAGATACGCCCTTTCTGAACACCAACAATGGCTACATC 1689

Qy 501 LeuSerHisProAspLeuArgProLeuTyrArgGluGlyLysLysLeuLysProLysPro 520
Db 1690 CHTCCCAATCCCGACCTCCGGCCCCCTGTACAGAGAGGGGAAGAACTAAACCCCAAACCT 1749
Qy 521 AsnTyrAsnSerValAspLeuSerGluValGluTrpGluAspGlnAlaGluSerLeuArg 540
Db 1750 AACTACAAACAGTGTGGATCTCTCCGAAGTGGAGTGGGAAGACCAGGCTGNAATCTCTGAGA 1809
Qy 541 ThrAlaMetIleAsnArgGluThrGlyThrLeuSerMetAspValLysValProMetAsp 560
Db 1810 ACAGCCATGATCAATAGGGAACAGGTACTCTCTCGATGGATGTGAAGGTTCGGATGGAT 1869
Qy 561 LysGlyLysArgValLeuPheLeuThrAsnAspTyrPhePheThrAspIleSerAspThr 580
Db 1870 AAGGGAACGGAGTTCTTTTCTTGACCAATGACTACTTCTTACGGACATCAGCGACACC 1929
Qy 581 ProPheSerLeuGlyAlaValLeuSerArgGlyHisGlyGluTyrIleLeuLeuGlyAsn 600
Db 1930 CTTTTTCAGTTTGGGGCGGTGCTCTCCGGGGCCACGGAGAATACATCCTTCTGGGGAAC 1989
Qy 601 ThrSerValGluGluGlyLeuHisAspLeuLeuHisProAspLeuAlaLeuAlaGlyAsp 620
Db 1990 ACGTCTGTGGAAAGAGCCCTGCATGACTTGTTCACCCAGACCTGGCCCTGGCCGGTGAC 2049
Qy 621 TrpIleTyrCysIleThrAspIleAspProAspHisArgLysLeuSerGlnLeuGluAla 640
Db 2050 TGGATCTACTGATCACAGATATTGACCCAGACCACCGGAAGCTCAGCCAGCTAGAGGCC 2109
Qy 641 MetIleArgPheLeuThrArgLysAspProAspLeuGluCysAspGluGluLeuValArg 660
Db 2110 ATGATCCGCTTCTTCACCAAGGAAGACCAGACCTGGAGTGTGACGAGAGCTGGTCCGG 2169
Qy 661 GluValLeuPheAspAlaValValThrAlaProMetGluAlaTyrTrpThrAlaLeuAla 680
Db 2170 GAGGTGCTGTTTGGACCGGTGTGACAGCCCCCATGGAAAGCCCTACTTGGGACGCGTGGCC 2229
Qy 681 LeuAsnMetSerGluGluSerGluHisValValAspMetAlaPheLeuGlyThrArgAla 700
Db 2230 CTCACATGTCGAGGAGTCTGNAACAGCTGGTGGACATGGCCCTTCTGGGCACCCGGGCT 2289
Qy 701 GlyLeuLeuArgSerSerLeuPheValGlySerGluLysValSerAspArgLysPheLeu 720
Db 2290 GGCTCTCTGAGAAGCAGCTTGTTCGTGGGCTCCGAGAAGGTCTCCGACAGGAAGTTCTTG 2349
Qy 721 ThrProGluAspGluAlaSerValPheThrLeuAspArgPheProLeuTrpTyrArgGln 740
Db 2350 ACACCTGAGGACGAGCGCCAGCGTGTTCACCTTGGACCCGCTTCCCGTGTGGTACCCGCCAG 2409
Qy 741 AlaSerGluHisProAlaGlySerPheValPheAsnLeuArgTrpAlaGluGlyProGlu 760
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Qy 761 SerAlaGlyGluProMetValValThrAlaSerThrAlaValAlaValThrValAspLys 780
Db 2470 AGTGGCGGTGAACCATGTGTGTGCGGCAAGCACAGCTGTGGCGGTGACCGTGGACAAG 2529
Qy 781 ArgThrAlaIleAlaAlaIleGlyValGlnMetLysLeuGluPheLeuGlnArgLys 800
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Qy 801 PheTrpAlaAlaThrArgGlnCysSerThrValAspGlyProTyrThrGlnSerCysGlu 820
Db 2590 TTCTGGCGGGCAACCGCGCAGTGCAGCATGTGGATGGCCGTACACACAGAGCTGGAG 2649
Qy 821 AspSerAspLeuAspCysPheValIleAspAsnAsnGlyPheIleLeuIleSerLysArg 840
Db 2650 GACAGTGATCTGGACTGCTTCGTTCATTCGACAAACAACGGGTTCATTTCTGATCTCCAAGAG 2709
Qy 841 SerArgGluThrGlyArgPheLeuGlyValAspGlyAlaValLeuThrGlnLeuLeu 860
Db 2710 TCCCAGAGACGGGAAGATTTCTGGGGGAGGTGGATGGTGTCTCTGACCCAGCTGCTC 2769

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Qy 861 SerMetGlyValPheSerGlnValThrMetTyrAspTyrGlnAlaMetCysLysProSer 880
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Qy 881 SerHisHisSerAlaAlaGlnProLeuValSerProIleSerAlaPheLeuThrAla 900
Db 2830 AGTCACACACAGTGCAGCCCGAGCCCTGGTCAGCCCAATTTCTGCCTTCTTGACGGCG 2889
Qy 901 ThrArgTrpLeuLeuGlnGluLeuValLeuPheLeuLeuGluTrpSerValTrpGlySer 920
Db 2890 ACCAGGTGGTGTCTGCAGGAGTGGTGTCTGCTCTGCTGAGTGGAGTGTCTGGGGTCTC 2949
Qy 921 TrpTrpAspArgGlyAlaGluAlaLysSerValPheHisHisSerHisLysLysLys 940
Db 2950 TGGTACGACAGAGGGCGGAGGCGCAAAAGTGTCTTCATCACTCCCAACAAACAAG 3009
Qy 941 GluAspProLeuGlnProCysAspThrGluTyrProValPheValTyrGlnProAlaIle 960
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Qy 961 ArgGluAlaAsnGlyIleValGluCysGlyProCysGlnLysValPheValValGlnGln 980
Db 3070 CGSGAGCCCAACGGGATCGTGGAGTGGCGCCCTGCCAGAGGTATTTGTGTGCGACGAG 3129
Qy 981 IleProAsnSerAsnLeuLeuValThrAspProThrCysAspCysSerIlePhe 1000
Db 3130 ATTCCCAACAGTAACCTCTCTCTCTGTCGACAGACCCACCTGTGACTGCAGCATCTTC 3189
Qy 1001 ProProValLeuGlnGluAlaThrGluValLysTyrAsnAlaSerValLysCysAspArg 1020
Db 3190 CCACCACTGTCTGCAGGAGGCGACAGAAAGTCAATATATATATGCTCTGTCAATGTGACCGG 3249
Qy 1021 MetArgSerGlnLysLeuArgArgProAspSerCysHisAlaPheHisProGluVal 1040
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Qy 1061 LeuCysProCysArgGlnGluHisIleGlyMetProMetAsnThrProValProValLeu 1080
Db 3370 CTGTGCCCTTGCAGACAGGAGCATATAGGATGCCAATGAACACACCTGTGCTGTGCTT 3429
Qy 1081 LeuGlyGlyAsnIleArgValTyrAlaLeu 1090
Db 3430 CTCGGGGGAAACATTCGCGTTTATGCCCTG 3459

RESULT 3
US-10-128-558-52
; Sequence 52, Application US/10128558
; Publication No. US20040219521A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Gezhi
; APPLICANT: Boyle, Bryan J
; APPLICANT: Drmanac, Radjoje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE OF INVENTION: Polypeptides
; FILE REFERENCE: 812A
; CURRENT FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: US/10/128,558
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: US 60/339,453
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
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; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: pt_FL_genes version 6.0
; SEQ ID NO 52
; LENGTH: 4841
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(3689)
US-10-128-558-52

Alignment Scores:
Pred. No.: 0 Length: 4841
Score: 5385.50 Matches: 1034
Percent Similarity: 97.47% Conservative: 5
Best Local Similarity: 97.00% Mismatches: 27
Query Match: 94.05% Indels: 1
DB: 21 Gaps: 0

US-09-833-222A-10 (1-1090) x US-10-128-558-52 (1-4841)

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Db 498 GAAACAGTGAAGCTATGGGCTGACACCTTCGGCGGGGACCTGTATAACACTGTGACCAA 557
Qy 31 TyrSerGlySerLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIle 50
Db 558 TACTCAGGCTCTCTCTTGTCTGCAGAAAGTACAAGATGTGGATCTCAGTCTGAAGATC 617
Qy 51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu 70
Db 618 GAGGAGGTGGATGGCTTGGAGCTGGTGAGGAGTCTCAGAGGACATGGAGAGACATGCTG 677
Qy 71 ArgArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsn 90
Db 678 CGGAGAAAGTGCAGGCGGTCCAGATCTGGTGAAGCTGCCGAGGAGCGGACCTGAAC 737
Qy 91 HisGluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArg 110
Db 738 CACGAATTCAATGAATCCCTGGTGTTCGACTATTACAACCTCGCTCTGTATCAACGAGAGG 797
Qy 111 AspGluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHis 130
Db 798 GACGAAAGGGCAACTTCGTGGAGCTGGGCGCGGAGTTCTCTCTGAGTCCAATGCTCAC 857
Qy 131 PheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyr 150
Db 858 TTCAGCAACTGCCGCTGAACACCTCCATCAGCAGCGTGCAGTCCCAACGCTGAC 917
Qy 151 AsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPhe 170
Db 918 AACAAAGACCCAGATATTTAAATGGAGTCTACATGTCTGAAGCCTTGAATGTGCTTTC 977
Qy 171 ValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGly 190
Db 978 GTGGAGAACTTCCAGAGAGACCCCAACGTTGACCTGGCAATATTTTGGCAGTGAACCTGGA 1037
Qy 191 PhePheArgIleTyrProGlyIleLysTyrTrpThrProAspGluAsnGlyValIleThrPhe 210
Db 1038 TTCTTCAGGATCTATCCAGGTATAAATGGACACCTGATCAGAAATGGAGTCAATCTTT 1097
Qy 211 AspCysArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIle 230
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Db	1098		GA	CTGCGGAAACCGCGGCTGCTACATTTCAAGCTGCTACTTCTCCCAAGGACATAGTGATT	1157
Qy	231		Leu	ValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIle	250
Db	1158		TTGG	TGGACGTGAGCGGCAGTATGAAGGGGCTGAGGATGACTATTGCAAGCACACCATC	1217
Qy	251		Thr	ThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyAsnAsp	270
Db	1218		ACCA	CCATCTTGACACCCCTGGGGGAGATGACTTCAATTAATATCATAGGCTCAATGAC	1277
Qy	271		Tyr	ValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsn	290
Db	1278		TACG	TCCATTACATCGAGCCTTGTTTTAAAGGATCCTCGTCAGGCGGACCGAGACAAT	1337
Qy	291		Arg	GluHisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAsp	310
Db	1338		CGAG	AGCATTTCAAACTGCTGGTGGAGGAGTTGATGGTCAAAAGGTGTGGGGTCTGGGAC	1397
Qy	311		Gln	AlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGlnAlaLysGlnGlySer	330
Db	1398		CAAG	CCCTGAGAGAGCCTTCCAGATCTCGAGCAGTTCCAAAGGCCCAAGCAAGGAGC	1457
Qy	331		Leu	CysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProVal	350
Db	1458		CTCT	GCAACCGGCCATCATGCTCATCAGCGACGGCGCGTGAGGACTACGAGCCGGTG	1517
Qy	351		Phe	GluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArg	370
Db	1518		TTTG	AAGATGATTAACCTGGCCAGACTGTGAAGTCCGAGTTTTCATTACCTCATTTGGGAGA	1577
Qy	371		Glu	ValSerPheAlaAspArgMetLysTyrIleAlaCysAsnAsnLysGlyTyrTyrThr	390
Db	1578		GAAG	TGCTTTGCTGACCCCATGAAGTGATTTGATGCAACCAACAAAGGCTACTACAG	1637
Qy	391		Gln	IleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSer	410
Db	1638		CAGAT	CTCAACGCTGGCGGACACCCAGGAGAACGTGATGAATACCTGCGACGTGCTCAGC	1697
Qy	411		Arg	ProMetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSer	430
Db	1698		CGCC	CCCATGCTCATCAACCAACGACCAACACATCATCTGGACAGAGCCCTACATGGACAGC	1757
Qy	431		Lys	LeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProVal	450
Db	1758		AAGC	TCTCAGCTCGCAGGCTCAGAGCCTGACACTGCTCACCCTGTGGCCATGCCAGTC	1817
Qy	451		Phe	SerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp	470
Db	1818		TTCA	GCAAGAAGAAACGAAACCGCATCCCATGGCATTCCTCTGGGTGTGGTGGGCTCAGAT	1877
Qy	471		Val	AlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyr	490
Db	1878		GTGG	CCCTTGAGAGAGCTGATGAAGCTGGCGCCCGGTACAAAGCTTGAGGTGCAACGGATAC	1937
Qy	491		Ala	PheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr	510
Db	1938		GCCT	TTCTGNAACCAACAATGGCTACATCTCTCCATCCCACTCCGACCTCCGGCCCTGTAC	1997
Qy	511		Arg	GluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluVal	530
Db	1998		AGAG	GGGGAAGAAATATAAACCAACCTAACTACAACAGTGTGGATCTCTCCGAAGTG	2057
Qy	531		Glu	TrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr	550
Db	2058		GAGT	GGGAAGACAGAGCTGAATCTCTGAGAACAGCCATCATCAATAGGGAAACAGGTACT	2117
Qy	551		Leu	SerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn	570
Db	2118		CTCT	CCATGATGTGAAGGTTCGATGGAATAAAGGGAAGCGAGTTCTTTCTGACCAAT	2177
Qy	571		Asp	TyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg	590

Db	2178		GACT	ACTTCTTACCGGACATCAGCAGACCCCTTTTCAGTTTGGGGGTGGTGCTGCCGG	2237
Qy	591		Gly	HisGlyGluTyrIleLeuLeuGlyAenThrSerValGluGluGlyLeuHisAspLeu	610
Db	2238		GGCC	ACGAGAAATACATCTTCTGGGGAACACGCTCTGTGGAAGAGCCCTGCATGACTTG	2297
Qy	611		Leu	HisProAspLeuAlaLeuAlaGlyAspTyrIleTyrCysIleThrAspIleAspPro	630
Db	2298		CTTC	ACCCAGACTGGCCCTGGCCGCTGACTGGATCTACTGCATCACAGATATTGACCCA	2357
Qy	631		Asp	HisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspPro	650
Db	2358		GACCA	CCGGAAGCTCAGCCAGCTTAGAGGCCATGATCCGCTTCTCACCAGAAAGGACCCA	2417
Qy	651		Asp	LeuGluCysAspGluLeuValArgGluValLeuPheAspAlaValValThrAla	670
Db	2418		GACCT	GGATGTGACAGAGAGCTGGTCCGGGAGGTGCTGTTTACCGGGTGGTGCAGCC	2477
Qy	671		Pro	MetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisVal	690
Db	2478		CCCA	TGGAAGCCTACTGGACAGCGCTGGCCCTCAACATGTCCGAGGAGTCTGAACAGTG	2537
Qy	691		Val	AspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGly	710
Db	2538		GTGG	CATGGCCTTCTGGGCAACCCGGGCTGGCCTCTCAGAAAGCAGCTTGTTCGTGGGC	2597
Qy	711		Ser	GluLysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThr	730
Db	2598		TCCG	AAGGCTCTCCACAGGAAGTTCTTGACACCTGAGGACAGGCCAGCGTGTCCACC	2657
Qy	731		Leu	AspArgPheProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheVal	750
Db	2658		CTGG	ACCGTGTGGTACCGCCAGGCTCTCAGAGCATCTCTGCTGGCAGCTTCGTC	2717
Qy	751		Phe	AsnLeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAla	770
Db	2718		TTCA	ACCTCCGCTGGGCGAAGAACCAAGAAAGTGGGGTGAACCCCATGTGTGTGACGGCA	2777
Qy	771		Ser	ThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAlaAlaGlyVal	790
Db	2778		AGCA	CAGCTGTGGCGGTGACCGTGGAACAAGAGACAGCCATTGCTGCAGCCGGCGGCTC	2837
Qy	791		Gln	MetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThr	810
Db	2838		CAAA	TGAAGCTGGAATTTCTCCAGCGCAATTTCTGGCGCGCAACGCGGAGTGCAGACT	2897
Qy	811		Val	AspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAsp	830
Db	2898		GTGG	ATGGGCCCGTGCACACAGAGCTCGAGGACAGTGATCTGGACTGCTTCTGTCATCGAC	2957
Qy	831		Asn	AsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGlu	850
Db	2958		AACA	CGGGTTTCATTTCTGATCTCCAAGAGTCCCAGAGACCGGAAGATTTCTGGGGAG	3017
Qy	851		Val	AspGlyValaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMet	870
Db	3018		GTGG	ATGGTGTGCTCTCTGACCCAGCTGCTCAGCATGGGGGTGTTCAGCAAGTACTATG	3077
Qy	871		Tyr	AspTyrGlnAlaMetCysLysProSerSerHisHisSerAlaAlaGlnProLeu	890
Db	3078		TATG	ACTATCAGGCCATGTGCAAAACCTCGAGTCACACACAGTGCAGCCGACCCCTG	3137
Qy	891		Val	SerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValLeu	910
Db	3138		GTCA	GGCCCAATTTCTGCCCTTTTGACGGCGAACAGGTGCTGCTGCAGAGCTGGTGTG	3197
Qy	911		Phe	LeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSer	930
Db	3198		TTCT	CTGTGAGTGTGAGTGTCTGGGCTCTCTGTTACGACAGAGGGGCCGAGGCCAAAGT	3257
Qy	931		Val	PheHisHisSerHisLysLysLysGlnAlaAspProLeuGlnProCysAspThrGlu	950
Db	3258		GTCT	TTCATCTCCACAAACACAAAGACAGGACCCCGCTGCAGCCCTGCGACACGGAG	3317

Qy 951 TyrProValPheValTyrGlnProAlaIleArgGluAlaAenGlyIleValGluCysGly 970
Db 3318 TACCCCGTGTTCGTACACCGCGCCATCCGGAGGCGCAACGGGATCGTGGAGTGGCGG 3377
Qy 971 ProCysGlnLysValPheValValGlnGlnIleProAenSerAenLeuLeuVal 990
Db 3378 CCCTGCCAAGAGGTATTTGTGGTCAGCAGATTCCTCCACAGATAACCTCTCTCTGTG 3437
Qy 991 ThrAapProThrCysAapCysSerIlePheProValLeuGlnGluAlaThrGluVal 1010
Db 3438 ACAGACCCCACTGTGACTGAGCATCTTCCACCACTGCTGCAGGAGCCACAGAGTC 3497
Qy 1011 LysTyrAenAlaSerValLysCysAapArgMetArgSerGlnLysLeuArgArgPro 1030
Db 3498 AATATAATGCTCTGTCAATGTGACCGGATGGCTCCACAGAGCTCCGCGCGCACCA 3557
Qy 1031 AspSerCysHisAlaPheHisProGluValArgValGluAlaAapArgGlyTrpAlaGly 1050
Db 3558 GACTCCTGCCAGCGCTTCCATCCAGAGGAGAAATGCCAGGACTCGCGCGCGCTCGGAC 3617
Qy 1051 PheSerSerProAenProLeuCysLeuGlyLeuCysProCysArgGlnGluHisIleGly 1070
Db 3618 ACCTCAGGCTCGCGCGCTTCTCTGCT-GCTGTGTGTGCTCGGGGCTACTGCCCA 3676
Qy 1071 MetProMetAenThrPro 1076
Db 3677 ACTCCTCGGTGCACACCA 3694

RESULT 4

US-10-257-174-10
; Sequence 10, Application US/10257174
; Publication No. US20040034194A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoying
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50022
; CURRENT APPLICATION NUMBER: US/10/257,174
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: PCT/US01/11797
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/196,603
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/199,417
; PRIOR FILING DATE: 2000-04-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 3228
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-257-174-10

Alignment Scores:

Pred. No.:	0	Length:	3228
Score:	5234.50	Matches:	1013
Percent Similarity:	95.68%	Conservative:	7
Best Local Similarity:	95.03%	Mismatches:	34
Query Match:	91.42%	Indels:	13
DB:	19	Gaps:	3

US-09-833-222a-10 (1-1090) x US-10-257-174-10 (1-3228)

Qy 12 ArgValLysLeuTrpAlaAapThrPheGlyGlyAapLeuTyrAenThrValThrLysTyr 31
Db 58 AGAGTGAAGCTATGGGCTGACACCTTCGGCGGGGACCTGTATAACACTGTGACCAATAC 117
Qy 32 SerGlySerLeuLeuGlnLysLysTyrLysAapValGluSerSerLeuLysIleGlu 51

Db 118 TCAGGCTCTCTTTGTCGAGAAAGTACAAAGATGTGGAGTCCAGTCTCAAGATCGAG 177
Qy 52 GluValAapGlyLeuGluLeuValArgLysPheSerGluAapMetGluAenMetLeuArg 71
Db 178 GAGGTGATGGCTTGGAGCTGGTGAGGAGTTCTCAGAGGACATGGAGAAACATGCTGGG 237
Qy 72 ArgLysValGluAlaValGlnAenLeuValGluAlaAaGluGluAlaAapLeuAenHis 91
Db 238 AGGAAAGTCGAGGCGGTCCAGAAATCTGGTGAAGCTGCCGAGGAGGCGGACCTCAACAC 297
Qy 92 GluPheAenGluSerLeuValPheAapTyrTyrAenSerValLeuIleAenGluAap 111
Db 298 GAATTCATGAATCCCTGGTGTTCGACTATTACAACTCGGTCTGTATCAACAGAGGAC 357
Qy 112 GluLysGlyAenPheValGluLeuGlyAlaGluPheLeuLeuGluSerAenAlaHisPhe 131
Db 358 GAGAAAGGCAACTTTCTGGTGGAGCTGGCGCGGAGTTCTCTCTGGAGTCCAATGCTCAC 417
Qy 132 SerAenLeuProValAenThrSerIleSerSerValGlnLeuProThrAenValTyrAen 151
Db 418 AGCAACCTGCGGTGAACACCTCCATCAGCAGCGTGCAGCTGCCACCAACGCTGTACAC 477
Qy 152 LysAapProAapIleLeuAenGlyValTyrMetSerGluAlaLeuAenAlaValPheVal 171
Db 478 AAGACCCAGATATTTTAAATGGAGTCTACATGTCGAAGCCTTGAATGCTCTCTCTG 537
Qy 172 GluAenPheGlnArgAapProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhe 191
Db 538 GAGAACTTCCAGAGACACCCAAACGTTGACCTGGCAATATTTTGGCAGTGAACCTGATTC 597
Qy 192 PheArgIleTyrProGlyIleLysTrpThrProAapGluAenGlyValIleThrPheAap 211
Db 598 TTCAGGATCTATCCAGGTATAAAATGGACACCTCATGAGAATGGAGTCATTACTTTTGC 657
Qy 212 CysAapAenArgGlyTrpTyrIleGlnAlaAaThrSerProLysAapIleValIleLeu 231
Db 658 TGCCGAAACCGCGCTCGTACATTCAGCTGCTACTTCTCCAAAGGACATAGTGAATTTG 717
Qy 232 ValAapValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThr 251
Db 718 GTGGAGTGAAGCGCAGTATGAAGGGCTGAGGATGACTATTGCCAAGCACCATCACC 777
Qy 252 ThrIleLeuAapThrLeuGlyGluAenAapPheValAenIleIleAlaTyrAenAapTyr 271
Db 778 ACCATCTTGGACACCTTGGGGGAGATGACTTCATTATATCATAGGCTACAAATGACTAC 837
Qy 272 ValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAapAaTqAapAenArg 291
Db 838 GTCCATTACATCGAGCCCTTGTTTTAAAGGATCTCTGTCAGGCGGACCCGAGACAATCGA 897
Qy 292 GluHisPheLysLeuLeuValGluLeuMetValLysGlyValValValValAapGln 311
Db 898 GAGCATTTCAAACTGCTGGTGGAGGAGTTCATGTCGTCAAAGGTGTGGGGTCTGTGACCA 957
Qy 312 AlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGlnAlaLysGlnGlySerLeu 331
Db 958 GCCCTCAGAGAAGCCTTCCAGATCCTGAAGCAGTTCCAAGAGGCGCAAGGAGGAGCTC 1017
Qy 332 CysAenGlnAlaIleMetLeuIleSerAapGlyValAValGluAapTyrGluProValPhe 351
Db 1018 TGCAACCCAGGCCCATCTGCTCATCAGCGCGCGCCGTGGAGGACTACGAGCCCGTGT 1077
Qy 352 GluLysTyrAenTrpProAapCysLysValArgValPheThrTyrLeuIleGlyArgGlu 371
Db 1078 GAGAGTATAACTGGCCAGACTGTAAAGTCCGAGTTTCTACTTACCTCATTTGGGAGAGA 1137
Qy 372 ValSerPheAlaAapArgMetLysTrpIleAlaCysAenAenLysGlyTyrTyrGln 391
Db 1138 GTGTCTTTTCTGACCGCATGAAGTGGATTGCAATGCAACCAACAAAGGCTACTACACGAG 1197
Qy 392 IleSerThrLeuAlaAapThrGlnGluAenValMetGluTyrLeuHisValLeuSerArg 411
Db 1198 ATCTCAACGCTGGCGGACCCAGGAGAACGTGATGGAATACCTGCACTGCTCAGCGCGC 1257

412 ProMetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSerLys 431
Db 1258 CCATGGTCAATCAACACGACCGCATCATCTGGACAGAGCCCTACATGGACAGCAAG 1317
Qy 432 LeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrValAlaMetProValPhe 451
Db 1318 CTCCTCAGCTCGCAGGCTCAGAGCTGACACTGCTCACCACCTGTGGCCATGCCAGTCTTC 1377
Qy 452 SerLysIleAsnGlnThrArgSerHisGlyIleLeuLeuGlyValValGlySerAspVal 471
Db 1378 AGCAAGAAGAACCAACCGCATCCCATGGCATTTCTCTGGGTGTGGTGGCTCAGATGTG 1437
Qy 472 AlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyrAla 491
Db 1438 GCCTTGAGAGAGCTGATGAAGCTGGCCGCCCGGTACAGCTTGGAGTGACAGATAGGCC 1497
Qy 492 PheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyrArg 511
Db 1498 TTTCTGAACACCAACATGCTACATCTCTCCATCCCGACCTCCGGCCCTGTACAGA 1557
Qy 512 GluGlyLysLysLysProLysProAsnTyrAsnSerValAspLeuSerGluValGlu 531
Db 1558 GAGGGGAAGAACTAAACCCAAACCTTAACACAGAGTGGATCTCTCCGAAGTGGAG 1617
Qy 532 TrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThrLeu 591
Db 1618 TGGGAAGACCCAGGCTGAATCTCTGAGAACAGCCATGATCAATAGGGAACAGGTACTCTC 1677
Qy 552 SerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsnAsp 571
Db 1678 TCGATGGATGTGAAGGTTCGATGGATAAAGGAAGCGAGTCTTTTCTCTGACCAATGAC 1737
Qy 572 TyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArgGly 591
Db 1738 TACTCTTTCACGACATCAGCGACACCCCTTTCAGTTTGGGGGTGGTGTCTCCCGGGC 1797
Qy 592 HisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeuLeu 611
Db 1798 CACGGAGATACATCTCTTCGGGAAACAGCTCTGTGGAGAGGCGCTGCATGACTTGCYT 1857
Qy 612 HisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspProAsp 631
Db 1858 CACCCAGACCTGGCCCTGGCCGCTGACTGGATCTACTGTCATCACAGATATTGACCCAGAC 1917
Qy 632 HisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspProAsp 651
Db 1918 CACCGGAAGCTCAGCCAGCTAGAGGCCATGATCCGCTTCTCCACGGAAGGACCCAGAC 1977
Qy 652 LeuGluCysAspGluGluLeuValArgGluValLeuPheAspAlaValValThrAlaPro 671
Db 1978 CTGGAGTGTGACAGGAGCTGGTCCGGAGGTGCTGTTTGACCGGTGTGACAGCCCCC 2037
Qy 672 MetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisValVal 691
Db 2038 ATGGAAGCCTACTGGACAGCGCTGGCCCTCAACATGTCCGAGGAGTCTGAACACGTGGT 2097
Qy 692 AspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGlySer 711
Db 2098 GACATGGCCCTCTCTGGGCACCCGGCTGGCTCTCTGAGAGCAGCTTGTTCGTGGGCTCC 2157
Qy 712 GluLysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThrLeu 731
Db 2158 GAGAAGGTCTCCGACAGGAAGTTCTTGACACTTGAGGACGAGGCCAGCGTGTACCCCTG 2217
Qy 732 AspArgPheProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheValPhe 751
Db 2218 GACCGCTTCCCGCTGTGTGTTACCGCCAGCGCTCAGAGCATCTCTGCTGGCAGCTTCGTCTTC 2277
Qy 752 AsnLeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAlaSer 771
Db 2278 AACCTCCGCTGGGAGAAAGACAGAAAGTGCGGGTGAACCCATGGTGGTGACGGCAAGC 2337

772 ThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAlaAlaAlaGlyValGln 791
Db 2338 ACAGCTGTGGCGGTGACCGTGGACAAGAGACAGCCATTGCTGCAGCCCGGGCGTCCAA 2397
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Qy 812 AspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAspAsn 831
Db 2458 GATGGCCCTGTCACACAGAGCTCGGAGGACAGTGATCTGGACTGCTTCTCATCGACAAC 2517
Qy 832 AsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGluVal 851
Db 2518 AACGGGTTCATTCTGATCTCCAAGAGTCCCAGAGACGGGAAGATTTCTCTGGGGAGGTG 2577
Qy 852 AspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMetTyr 871
Db 2578 GATGGTGTCTGCTGACCCAGCTGCTCAGACTGGGGGTGTTTCAGCCAAGTGACTATGTAT 2637
Qy 872 AspTyrGlnAlaMetCysLysProSerSerHisHisSerAlaAlaGlnProLeuVal 891
Db 2638 GACTATCAGCCATGTGCAACCCCTCGAGTCACCAACAGTCAGCCAGCCCTTGCTC 2697
Qy 892 SerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValPhe 911
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Qy 912 LeuLeuGluTyrSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSerVal 931
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Qy 932 PheHisHisSerHisLysHisLysGlnAspProLeuGlnProCysAspThrGluTyr 951
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Db 2917 TGCCAGAGGTATTTGTGTGACAGAGATTCCCAACAGTAACCTCTCTCTCTGGTGACA 2976
Qy 992 AspProThr--CysAspCysSerIlePheProValLeuGlnGluAlaThrGluVal 1010
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Qy 1011 LysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgArgPro 1030
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Db 3097 GACTCTGTCAGCCCTTCCATCCAGAGGAAGATGCCAGGAGCTGCGCGCGCTCGGAC 3156
Qy 1051 PheSerSerProAsnProLeuCysLeuGlyLeuCysProCysArgGlnGluHisIleGly 1070
Db 3157 ACCTGAGCTCGCGGCCCTTCTCTGCT--GCCTGTGTGTGC-----CTGGGG 3203
Qy 1071 MetProMetAsnThrPro 1076
Db 3204 GCTACTGCCCCCACTCTCT 3221
RESULT 5
US-10-257-174-11
; Sequence 11, Application US/10257174
; Publication No. US20040034194A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.

Db 1912 GGCACGAGAAATACATCTTCTGGGAAACAGCTCTGTGGAGAGGCGCTGCATGACTTG 1971
Qy 611 LeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspPro 630
Db 1972 CTTTACCCAGACCTGGCCCTTGGCCGCTGACTGGATCTTACTGTCATCAGATATTGACCCA 2031
Qy 631 AspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspPro 650
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Qy 691 ValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGly 710
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Db 2512 CAAATGAAGCTGAATTTCTCCAGCGCAAAATTTCTGGCGCGCAACGGCGGAGTGCAGCACT 2571
Qy 811 ValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAsp 830
Db 2572 GTGGATGGGCGGTGCACACAGAGCTCGAGAGCAGTGAICTGACACTGCTTCGTGTCATCGAC 2631
Qy 831 AsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGlu 850
Db 2632 AACAAACGGGTTCATTCTGATCTCCAAGAGGTCCCGAGAGACGGGAAGATTTCTGGGGGAG 2691
Qy 851 ValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMet 870
Db 2692 GTGGATGGGTGCTGCTGACCCAGCTGCTCAGATGGGGGTGTTACGCCAAGTACATATG 2751
Qy 871 TyrAspTyrGlnAlaMetCysLysProSerSerHisHisSerAlaAlaGlnProLeu 890
Db 2752 TATGACTATCAGGCCATGTGCAAACCTCGAGTCAACACACAGTCAGCCAGCCGCCCTG 2811
Qy 891 ValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluValLeu 910
Db 2812 GTCAGGCCAAATTTCTGCTTCTTGAACGGGACCCAGGTGGCTGTGTCAGGAGCTGGTGTG 2871
Qy 911 PheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSer 930
Db 2872 TTCCTGCTGAGTGGAGTGTCTGGGCTCTCTGTGTACGACAGAGGGGCCGAGGCC----- 2925
Qy 931 ValPheHisSerHisLysHisLysGlnAspProLeuGlnProCysAspThrGlu 950
Db 2926 -----CACAAACACAGAGAGCAGGACCCGCTGCAGCGCTGCAGACGGAG 2970
Qy 951 TyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGly 970

Db 2971 TACCCTGCTGTCTGTGTACCAAGCGGCCATCCGGAGGCCCAACGGGATCGTGGAGTGGGG 3030
Qy 971 ProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLeuLeuVal 990
Db 3031 CCTGTCAGAGGTATTTGTGGTGCAGCAGATTCCCAACAGTAACCTCTCTCTCTCTCTG 3090
Qy 991 ThrAspProThr---CysAspCysSerIlePheProValLeuGlnGluAlaThrGlu 1009
Db 3091 ACAGACCCCACTTCTGAGATGGCTCGGCTCGGCTCTGAGATATTGACCTTAACAGTGGCT 3150
Qy 1010 ValLysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgArg 1029
Db 3151 TCTGCACATAATGCTCTCTCAAAATGTGACCGGATGCGCTCCCGAAGCTCCGCGCGCA 3210
Qy 1030 ProAspSerCysHisAlaPheHisProGluValArgValGluAlaAspArgGlyTrpAla 1049
Db 3211 CCAGACTCTCTGCACGCTTTCATCCAGAGGAATGCCAGGACTGCGCGCGCTCG 3270
Qy 1050 GlyPheSerSerProAsnProLeuCysLeuGlyLeuCysProCysArgGlnGluHisIle 1069
Db 3271 GACACTCAGCTCGCGGCTCTCTCTGCT-GCCTGTGTGTGC-----CTG 3317
Qy 1070 GlyMetProMetAsnThrPro 1076
Db 3318 GGGGCTACTGCCCAACTCT 3338
RESULT 6
US-10-257-022-27
; Sequence 27, Application US/10257022
; Publication NO. US20030211499A1
; GENERAL INFORMATION:
; APPLICANT: REDDY, Roopa
; APPLICANT: THORNTON, Michael
; APPLICANT: BOROWSKY, Mark L.
; APPLICANT: TANG, Y. Tom
; APPLICANT: KHAN, Farrah A.
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: YAO, Monique G.
; APPLICANT: SANJANWALA, Madhusudan M.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: NGUYEN, Dannie B.
; APPLICANT: POLICKY, Jennifer L.
; APPLICANT: YUE, Henry
; APPLICANT: SEILHAMER, Jeffrey J.
; APPLICANT: WALIA, Narinder K.
; APPLICANT: LAL, Preeti
; APPLICANT: KEARNEY, Liam
; APPLICANT: WALSH, Roderick T.
; APPLICANT: LU, Dying Aina M.
; APPLICANT: LU, Yan
; APPLICANT: GREENE, Barrie D.
; APPLICANT: RAUMANN, Brigitte E.
; APPLICANT: Arvizu, Chandra S.
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: PI-0067 USN
; CURRENT APPLICATION NUMBER: US/10/257,022
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: US01/11206
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/195,595
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/196,872
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/199,020
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/200,552
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/202,348
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/203,495
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 30


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Db 3040 TACGCCCTTCTGAACACCAATGGGTACATCTCTCCATCCCGACCTCCGGCCCGCTG 3099
Qy 510 TyArgGluGlyIleLysLeuLeuProLysProLysProAsnTyrAsnSerValAspLeuSerGlu 529
Db 3100 TACAGAGAGGGGAAGAAATAAACCACCACTTAACCTACAACTGATGATGATCTCCGAA 3159
Qy 530 ValGluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGly 549
Db 3160 GTGGAGTGGGAAGACCAAGGCTGATCTCTGAGAACGCCATGATCAATAGGGAACAGGT 3219
Qy 550 ThrLeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThr 569
Db 3220 ACTCTCTCGATGGATGGAGTTCCGATGGATAAAGGAAGCGAGTTCTTTTCCTGACC 3279
Qy 570 AsnAspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSer 589
Db 3280 AATGACTACTTCTTCCGAGCATCAGCGACACACCCCTTTTCAGTTTGGGGTGGTGCTGCC 3339
Qy 590 ArgGlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAsp 609
Db 3340 CGGGGCCACGAGAAATACATCTTCTGGGGAACACGCTCTGTGAAGAAGGCCCTGCATGAC 3399
Qy 610 LeuLeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAsp 629
Db 3400 TTGCTTCCACCCAGACTTGGCGCCCTGGCGGGTACTGGATCTACTGCATCACAGATATGAC 3459
Qy 630 ProAspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAsp 649
Db 3460 CCAGACCACCGGAAGCTACCCAGCTAGAGGCCATGATCGCTTCTCCACGAGGAGGAC 3519
Qy 650 ProAspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAlaValThr 669
Db 3520 CCAGACCTGGAGTGTGACGAGGAGCTGGTCCGGGAGGTGCTGTGTACCGCGTGTGACA 3579
Qy 670 AlaProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHis 689
Db 3580 GCCCCCATGGAAGCCTACTGGACAGCGCTGGCCCTCAACATGTCCGAGGAGTCTGAACAC 3639
Qy 690 ValValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheVal 709
Db 3640 GTGGTGGACATGCGCTTCTTGGGCACCCGGGCTGGCTCTCGAGAGCAGCTTGTTCGTG 3699
Qy 710 GlySerGluLysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPhe 729
Db 3700 GGCTCCGAGAAGGTCTCCGACAGGAAGTTCTCTGACACCTGAGGACGAGCGCAGGTGTTTC 3759
Qy 730 ThrLeuAspArgPheProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPhe 749
Db 3760 ACCCTGGACCGCTTCCGCTGTGGTACCGCCAGCGCTCAGAGCATCCTGCTGGCAGCTTC 3819
Qy 750 ValPheAsnLeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThr 769
Db 3820 GTCTTCAACCTCGCTGGCGGAGAGGACCA-----GGACGCCCTTCTGCCAAAGGC 3870
Qy 770 AlaSerThrAlaValAlaValThrValAspLysArg 781
Db 3871 CTTCCACCACCACTTTTGCCAAACCATCTCTCAAGCGT 3906
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RESULT 7

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US-10-924-081-5
; Sequence 5, Application US/10924081
; Publication No. US20050095678A1
; GENERAL INFORMATION:
; APPLICANT: PARKER, David
; APPLICANT: XU, Xianghong
; APPLICANT: KHAWAJA, Afreen
; APPLICANT: SNUATCH, Terrance P.
; TITLE OF INVENTION: NOVEL RAT CALCIUM CHANNEL SUBUNITS AND
; TITLE OF INVENTION: RELATED PROBES, CELL LINES AND METHODS
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; FILE REFERENCE: 381092001400
; CURRENT APPLICATION NUMBER: US/10/924,081
; CURRENT FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: PCT/CA2004/001550
; PRIOR FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: US 60/497,096
; PRIOR FILING DATE: 2003-08-22
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3598
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-924-081-5

Alignment Scores:
Pred. No.: 0 Length: 3598
Score: 3422.50 Matches: 626
Percent Similarity: 77.54% Conservative: 192
Best Local Similarity: 59.34% Mismatches: 220
Query Match: 59.77% Indels: 18
DB: 22 Gaps: 6
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US-09-833-222A-10 (1-1090) x US-10-924-081-5 (1-3598)

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Qy 13 ValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLysTyrSer 32
Db 124 GTGAAGCTCTGGCCCTCCGCTTTTGGTGGGGAGATAAAATCCATTGCTGCCAAGTACTCG 183
Qy 33 GlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIleGluGlu 52
Db 184 GGTTCACGCTTCTGCAAAAGAAATACAAAGAGTATGAGAAAGACGCTTGCCATTGAAGAA 243
Qy 53 ValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArgArg 72
Db 244 ATCGACGGTCTCCAACTGGTGAAAAAGCTGGGCCAAGAACATGGAAGAGATGTTTCAAG 303
Qy 73 LysValGluAlaValGlnAsnLeuValGluAlaGluGluAlaAspLeuAsnHisGlu 92
Db 304 AAGTCGAGGAGAGTGGCGGCTCTCGTGGAGGCTGCAGAGAGACACACCTGAAGCATGAA 363
Qy 93 PheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArgAspGlu 112
Db 364 TTTGACGCGCAGCTGCAGTATGAATACTTCAATGCCGTCTGATCAACGAGAGACAAA 423
Qy 113 LysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHisPheSer 132
Db 424 GATGGGAACCTTTTGGAAATTTGGAAAGGAGTTTCATCTTGGCCCCCAATGACCATTTAAT 483
Qy 133 AsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyrAsnLys 152
Db 484 AATTTGCCCTGTGAAACATCAGTCTGAGTGTGTCGAAGTCCCAAGTCCCAACGATGTACA 543
Qy 153 AspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPheValGlu 172
Db 544 GATCCTGCCATAGTCAATGGAGTGTATTGGTCTGAATCTCTAAACAAAAGTTTTTGTAGAC 603
Qy 173 AsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhePhe 192
Db 604 AACTTCGATCGGGACCCGCTCTCTCATATGGCAGTAGTCTTTGGAAGTGCAAGGGCTTTTC 663
Qy 193 ArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPheAspCys 212
Db 664 AGACAGTACCCAGGAGTTAAATGGGAACCAAGACAGAGATGGAGTCAATGCCCTTTGACTGC 723
Qy 213 ArgAsnArgGlyTrpTrpIleGlnAlaAlaThrSerProLysAspIleValIleLeuVal 232
Db 724 AGGAACAGGAAATGGTACATCCAGGAGCAACTTCTCCAAAGGATGTGTCATCTTTGGTG 783
Qy 233 AspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThrThr 252
Db 784 GACGTGACGGGAGCATGAAAGGACTCCGCTTGACCATGCGCAAGCAACAGTCTCCTCG 843
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Db 2971 TGTGAAGACTGCTCAAGTCTTTGTCTCATCCAGCAAAATCCAAAGTAGCAATCTGTTTCATG 3030
Qy 989 LeuValThrAspProThrCysAspCysSerIlePheProValLeuGlnGluAlaThr 1008
Db 3031 GTGGTGGTGACAGTAGCTGCTCTGTGAGTCTGTGGCTCTCTATCCACCATGGCACCCATT 3090
Qy 1009 GluValLysTyrAenAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgArg 1028
Db 3091 GAAATCAGGTATATGAATCCCTTAAGTGTGAACGGTTAAAGGCTCAGAAGATCAGACGA 3150
Qy 1029 ArgProAspSerCysHisAlaPheHisProGluValArgValGluAlaAspArgGlyTyr 1048
Db 3151 CGTCCGAATCCGCCACGGCTTCCATCTCTGAGGA-----GAAATGCCAGAGAGTGTGG 3203
Qy 1049 AlaGlyPheSerProAenProLeuCysLeuGlyLeuCysPro 1063
Db 3204 GGGTGCATCAAGTCTCCAGGCCCCAGGTGGCCTTGTGCTGCTGCC 3248

RESULT 8

US-09-728-628-12
; Sequence 12, Application US/09728628
; Patent No. US20020009786A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Ren, Feiyan
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20020009786A1el Nucleic Acids and
; FILE OF INVENTION: Polypeptides
; CURRENT APPLICATION NUMBER: US/09/728, 628
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 09/552,929
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 12
; LENGTH: 3528
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (213)..(3206)
US-09-728-628-12

Alignment Scores:
Pred. No.: 0 Length: 3528
Score: 3421.50 Matches: 629
Percent Similarity: 77.83% Conservative: 189
Best Local Similarity: 59.85% Mismatches: 212
Query Match: 59.75% Indels: 22
DB: 9 Gaps: 7

US-09-833-222A-10 (1-1090) x US-09-728-628-12 (1-3528)

Qy 12 ArgValLysLeuThrAlaAspThrPheGlyAspLeuTyrAsnThrValThrLysTyr 31
Db 51 AGGGTGAAGCTCTGGGCTCGGCTTTGGTGGGAGATAAAATCCATTGCTGCTAAGTAC 110
Qy 32 SerGlySerLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysLysGlu 51
Db 111 TCCGGTTCCAGCTTCTGCAAAAGAAATACAAAGAGTATGAGAAAGACGTTGCCATAGAA 170
Qy 52 GluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArg 71
Db 171 GAAATCGATGGCTCCAACTGGTAAAGAGCTGGCAAGAACATCGAAGAGATGTTTCAC 230

Qy 72 ArgLysValGluAlaValGlnAenLeuValGluAlaAalGluGluAlaAsePheLeuAenHis 91
Db 231 AAGAATCTGAGCCCTCAGGCGCTCTGGTGGAGCTGCGAAGAACACACACCTGAAACAT 290
Qy 92 GluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuLysLeuGluArgAsp 111
Db 291 GAATTTGATGCAGACTTACAGTATGAATACTTCAATGCTGTGCTGATTAATGAAGGAC 350
Qy 112 GluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHisPhe 131
Db 351 AAAGCGGGAATTTTGGAGCTGGGAAGGAATTCATCTTAGCCCAATGACCATTTT 410
Qy 132 SerAsnLeuProValAenThrSerIleSerSerValGlnLeuProThrAsnValTyrAsn 151
Db 411 AATAATTTGCTGTGAACATCAGTCTAAGTGAGCTCCAAGTACCAACGACATGTACAAC 470
Qy 152 LysAspProAspIleLeuAenGlyValTyrMetSerGluAlaLeuAenAlaValPheVal 171
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Qy 172 GluAenPheGlnArgAspProThrLeuThrTyrGlnTyrPheGlySerAlaThrGlyPhe 191
Db 531 GATACTTTGACCGTGACCCATCTCTCATATGCGAGTACTTTTGGAAAGTGAAGGGCTTT 590
Qy 192 PheArgIleTyrProGlyIleLysTyrThrProAspGluAenGlyValIleThrPheAsp 211
Db 591 TTTAGCAGTATCCGGGATTAATGGGAACACAGATGAGATGGAGTCATTGCTTCGAC 650
Qy 212 CysArgAsnArgGlyTyrTyrIleGlnAlaAlaThrSerProLysAspIleValIleLeu 231
Db 651 TGCAGAACCGAAATGGTACATCCAGGCGACAACTTCTCCGAAGACGTTGTCATTTA 710
Qy 232 ValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThr 251
Db 711 GTTGAGTCTGAGTGGCAGCATGAAGAGCTCCGTCGCTGCTATCCGGAAGCAACAGTCTCA 770
Qy 252 ThrIleLeuAspThrLeuGlyGluAenAspPheValAsnIleAlaTyrAsnAspTyr 271
Db 771 TCCATTTTGGATACACTTGGGGATGATGACTTCTTCAACATAATGCTTATATAGGAG 830
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Db 831 CTTCACTATGTGAACCTTGTCCCTGAATGGAACCTTTGGTGCAGCCGACAGGACAAACAA 890
Qy 292 GluHisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAspGln 311
Db 891 GAGCACTTCAGGAGGAGCATCTGGACAACTTTTCGCCAAGGAATGGAATGTTGGATATA 950
Qy 312 AlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySerLeu 331
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Qy 332 CysAsnGlnAlaIleMetLeuLysSerAspGlyAlaValGluAspTyrGluProValPhe 351
Db 1011 TGCAGTCAAGCCATCATGTCTATACTGATGGGCGGTGGACACCTATGATACAATCTTT 1070
Qy 352 GluLysTyrAsnTyrProAspCysLysValArgValPheThrTyrLeuLysGlyArgGlu 371
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Qy 372 ValSerPheAlaAspArgMetLysTyrIleAlaCysAsnAsnLysGlyTyrTyrThrGln 391
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Db 1191 ATCTCCACCTTGCTGATGTGCAGGAGATGTGATGGAATACCTTCCACGTCTTACCGG 1250
Qy 412 ProMetValIleAsnHisAspHisAspIleIleTyrThrGluAlaTyrMetAspSerLys 431
Db 1251 CCCAAGTCAATGCACGAGGATGATGTGGTGTGGACCGACGACTTACATTGACAGCACT 1310
Qy 432 LeuLeuSerSerGlnAlaGlnSerLeuThr-----LeuLeuThrThr 445

Db 1311 CTC-----CCTCAGGCACAAAAGCTGACTGATGATCAGGGCCCCCGTCTGATGACCACCT 1364
Qy 446 ValAlaMetProValPheSerLysLysAenGluThrArgSerHisGlyIleLeuLeuGly 465
Db 1365 GTAGCCATGCTGTGTTAGTAGCAGACAGAACCAACAGATCGAAGGGCATCTTCTGGGA 1424
Qy 466 ValValGlySerAspValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeu 485
Db 1425 GTGGTTGGCAGATGCTCCAGTGAAGAACTTCTGAAGACCCTCCCAATAACAAGTTA 1484
Qy 486 GlyValHisGlyTyrAlaPheLeuAenThrAsnAsnGlyTyrIleLeuSerHisProAsp 505
Db 1485 GGGATTCCAGGTTATGCTTTGCAATCACAATAATGGATATATCTCTGACGCATCCGGAA 1544
Qy 506 LeuArgProLeuTyrArgGluGlyLysLeuLysProLysProAsnTyrAsnSerVal 525
Db 1545 CTAGGCTGTGTACGAGAGGAGGAAAAG---CGAAGGAAACCTAATATAGTAGCGTT 1601
Qy 526 AspLeuSerGluValGluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsn 545
Db 1602 GACCTCTCTCAGGTGGAGTGGGAAGACCGAGATGACGTGTGAGAAATGCTATGGTGAAT 1661
Qy 546 ArgGluThrGlyThrLeuSerMetAspValLysValProMetAspLysGlyLysArgVal 565
Db 1662 CGAAAGACGGGGAAGTTTTCATCGAGGTGAAGAAGACAGTGGACAAAGGGAACGGGTT 1721
Qy 566 LeuPheLeuThrAsnAspTyrPhePheThrAspLysSerAspThrProPheSerLeuGly 585
Db 1722 TTGGTGAATGAATGACTACTATTTATACAGATCATCAGGGTACTCTCTTCAGTTTAGGT 1781
Qy 586 AlaValLeuSerArgGlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGlu 605
Db 1782 GTGGCGCTTTCCAGAGTCTATGGGAATAATTTCTCCGAGGGAATGTAACCATCGAAGAA 1841
Qy 606 GlyLeuHisAspLeuLeuHisProAspLeuAlaGlyAspTrpIleTyrCysIle 625
Db 1842 GGCTCTCATGACTTAGAACAATCCGATGTGCTCTGAGTGAAGAAATGATCCAAGAGTCCCTACTGCAAC 1901
Qy 626 ThrAspIleAspProAspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeu 645
Db 1902 ACTGACCTCACCTCAGCACCCCATCTCTCTCAGTTAAGCGATTAAGCTCTACCTA 1961
Qy 646 ThrArgLysAspProAspLeuGluCysAspGluLeuValArgGluValLeuPheAsp 665
Db 1962 AAAGGCAAGAACCTCTGCTCCAGTGTGATAAAGAAATGATCCAAGAGTCCCTTTTGAC 2021
Qy 666 AlaValValThrAlaProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGlu 685
Db 2022 GCGGTGGTGAAGTCCCGCATTTGAAGCGTATTTGGACCAAGCCTGGCCCTCAACAAATCTGAA 2081
Qy 686 GluSerGluHisValValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSer 705
Db 2082 AATTCAGACAGGCGTGGAGGTTCCTCTCGCACTCGACGGGCTCTCCGAATC 2141
Qy 706 SerLeuPheValGlySerGluLysValSerAspArgLysPheLeuThrProGluAspGlu 725
Db 2142 AACCTGTTTCTCGGGCTGAGCAGCTCACCAATCAGGACTTCTCTGAAAAGCTGGTGACAAG 2201
Qy 726 AlaSerValPheThrLeuAspArgPheProLeuTyrTrpArgGlnAlaSerGluHisPro 745
Db 2202 GAGAACATTTTAAACGCAGACCAATTTCCCTCTCTGTTACGGAAGAGCCGCTGAGCAGATT 2261
Qy 746 AlaGlySerPheValPheAenLeuArgTyrAlaGluGlyProGluSerAlaGlyGluPro 765
Db 2262 CCAGGAGACTTCTACTCGATCCCATTCAGCACTCGACCTGGACCA-----GTCAATAAAGC 2315
Qy 766 MetValValThrAlaSerThrAlaValAlaValThrValAspLysArgThrAlaIleAla 785
Db 2316 AATGTGTGACAGCAAGTATCATCCATCCATCCAGTCTCTGATGAACGGAAATCTCTGTGGTG 2375
Qy 786 AlaAlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLysPheThrAlaAlaThr 805

Db 2376 GCAGCTGTAGGCATTCAGATGAAACTTGAATTTTCCAAAGGAAGTTCTGGACTGCCAGC 2435
Qy 806 ArgGlnCysSerThrValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAsp 825
Db 2436 AGACAGTGTGCTCCCTGGATGGCAATGCTCCATCAGCTGTGATGATGAGACTGTGAAT 2495
Qy 826 CysPheValIleAspAenGlyPheIleLeuIleSerLysArgSerArgGluThrGly 845
Db 2496 TGTACTCATAGACAATAATGATTTATTTGGTGTCTGAAGACTACACAGACTGGA 2555
Qy 846 ArgPheLeuGlyValValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPhe 865
Db 2556 GACTTTTGGTGAGATCGAGGAGCTGTGATGAACAAATTTGTAACAATGGGCTCCTTT 2615
Qy 866 SerGlnValThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisSer 885
Db 2616 AAAAGAAATTACCTTTATGACTACCAAGCCATGTGTAGACCAACAAGGAAGACGCGAT 2675
Qy 886 AlaAlaGlnProLeuValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeu 905
Db 2676 GGCGCCCATGGCTCTGGATCCTTAATAGCCTCTCTCTGCAGTAAATAATGATCATG 2735
Qy 906 GlnGluLeuValLeuPheLeuGluTyrSerValTrpGlySerTrpTyrAspArgGly 925
Db 2736 ACAGAACTTGTCTGTGTGGTGAATTTAACTCTGC---AGTTGGTGGCACTCCGAT 2792
Qy 926 AlaGluAlaLysSerValPheHisHisSerHisLysLysGlnAspProLeuGln 945
Db 2793 ATCAGACAGCTAAAGCC-----CAGAAATTGAACACAGACCTCGAG 2831
Qy 946 ProCysAspThrGluTyrProValPheValTyrGlnProAlaIleArgGluAlaAenGly 965
Db 2832 CCTTGTGATACTGAATATCAGCATTCGCTCTGAGCGCACCATCAAGGAGACTACAGG 2891
Qy 966 IleValGluCysGlyProCysGlnLysValPheValValGlnGlnIleProAsnSerAsn 985
Db 2892 AATATTGCTGTGAAGACTGCTCAAGTCTCTTGTATCAGCAAAATCCCAAGCAGCAAC 2951
Qy 986 LeuLeuLeuLeuValThrAspProThrCysAspCysSerIlePheProValLeuGln 1005
Db 2952 CTGTTTCATGGTGGTGGACAGCAGCTGCTCTGTGAATCTCTGGCCCCCATCACCATG 3011
Qy 1006 GluAlaThrGluValLysTyrAenAlaSerValLysCysAepArgMetArgSerGlnLys 1025
Db 3012 GCACCATTTGAATCAGGTATAATGAATCCCTTAAGTGTGAACGCTCTAAAGGCCAGAG 3071
Qy 1026 LeuArgArgProAspSerCysHisAlaPheHisProGluValArgValGluAlaAsp 1045
Db 3072 ATCAGAAAGGCCCGCAGAACTTGTCTCATGCTTCCATCTCTGAG-----GAGAAATGCAAGG 3125
Qy 1046 ArgGlyTyrAlaGlyPheSerSerProAsnPro 1056
Db 3126 GAGTG-TGGGGTGGCCCGAGTCTCCAAAGCCCA 3157

RESULT 9
US-10-972-024-117
; Sequence 117, Application US/10972024
; Publication No. US20050221342A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 791CIP4
; CURRENT APPLICATION NUMBER: US/10/972,024
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: PCT/US01/08655
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/668,317
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/695,783

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; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 09/728, 628
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 09/783, 066
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 09/816, 828
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 584
; SOFTWARE: Custom
; SEQ ID NO 117
; LENGTH: 3528
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (213)..(3203)
US-10-972-024-117

Alignment Scores:
Pred. No.: 0 Length: 3528
Score: 3421.50 Matches: 629
Percent Similarity: 77.83% Conservative: 189
Best Local Similarity: 59.85% Mismatches: 212
Query Match: 59.75% Indels: 22
DB: 24 Gaps: 7

US-09-833-222A-10 (1-1090) x US-10-972-024-117 (1-3528)

QY 12 ArgValLysLeuTrpAlaAspThrPheGlyAspLeuTyrAsnThrValThrLysTyr 31
Db 51 AGGGTGAAGCTCTGGGCTCGGCTTTTGGTGGGAGATAAAATCCCATTCGTGCTAAGTAC 110
QY 32 SerGlySerLeuLeuGlnLysTyrLysAspValGluSerSerLeuLysIleGlu 51
Db 111 TCCGGTTCCTCCAGCTTCGCAAAAGAATAACAAGAGATGAGAAAAGACGTGCGCATAGAA 170
QY 52 GluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArg 71
Db 171 GAAATCGATGGCTCCAACTGGTAAAGAGCTGGCAAGAACATGGAAGAGATGTTTCAC 230
QY 72 ArgLysValGluAlaValGlnAsnLeuValGluAlaGluAlaAspLeuAsnHis 91
Db 231 AAGAAGCTCTGAGGCGCTCAGGCGTCTGGTGGAGGCTGCAGAAAGACACCTGGAACAT 290
QY 92 GluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArgAsp 111
Db 291 GAATTTGATCGACACTTACAGTATGAATACCTTCATGCTGCTGCTGATTAATGAAGGAC 350
QY 112 GluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHisPhe 131
Db 351 AAAGACGGGAATTTTGGAGCTGGGAAGGAATTCATCTTAGCCCCCAATGACCATTTT 410
QY 132 SerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyrAsn 151
Db 411 AATAATTTGGCTGTGAACATCATCTAAGTGACGTCCAAGTACCAACGAACATGTACAAC 470
QY 152 LysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPheVal 171
Db 471 AAGACCTTGCATTTGCAATGCTCAATGGGGTTATGGTCTGAATCTTAAACAAAGTTTGTGA 530
QY 172 GluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhe 191
Db 531 GATAACTTTTGACGTGACCCATCTCTCATATGGCAGTACTTTTGGAAAGTGCAAGGGCTTT 590
QY 192 PheArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPheAsp 211
Db 591 TTTAGGCAGTATCCGGGGATTAATGGGAACCAAGATGAGAATGGAGTCAATTCGCTTCGAC 650
QY 212 CysArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIleLeu 231
Db 651 TGCAGAACCGAAAATGGTATACATCCAGGCGACAACTTCTCCGAAAGCGTGGTCATTTTA 710
QY 232 ValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThr 251

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Db 711 GTTGAGCTCAGTGGCAGCATGAAGGACTCCGCTGACTATCGGAAGCAAAACAGTCTCA 770
QY 252 ThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAspTyr 271
Db 771 TCCATTTTGGATACACTTGGGGATGATGACTTCTTCAACATAATTCCTTATATATGAGGAG 830
QY 272 ValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsnArg 291
Db 831 CTTCACATATGTGAACCTTGCCTGAATGGAACCTTTGGTGAAGCCACGAGGACAACAA 890
QY 292 GluHisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAspGln 311
Db 891 GAGCAGCTTCAGGGAGCATCTGGACAAACTTTTCGCCAAAGGAATTCGAATGTTGGATATA 950
QY 312 AlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGlnAlaLysGlnGlySerLeu 331
Db 951 GCTCTGAATGAGGCTTCAACATTCCTGAGTGAATTCACACACACGCGGACAAGGAATTC 1010
QY 332 CysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProValPhe 351
Db 1011 TGCAGTCAAGCCATCATGCTCATTAAGTGGGCGGTGGACACCTATGATACAAATCTTT 1070
QY 352 GluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArgGlu 371
Db 1071 GCAAAATACAAATTGGCCAGATCGAAAGGTTCCGATCTTCATACATCTTCATGGACGAG 1130
QY 372 ValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThrGln 391
Db 1131 GCTGGTGTGCAGACAACTAAAGTGGATGGGCTGTGCCAACAAAGAGATTTTTTACCCAA 1190
QY 392 IleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSerArg 411
Db 1191 ATCTCCACCTTGGCTGATGTGCAGGAGATGTCATGGAATACCTTCACCTGCTTACCGCG 1250
QY 412 ProMetValIleAsnHisAspIleLeuIleTrpThrGluAlaTyrMetAspSerLys 431
Db 1251 CCCAAAGTCATCGACCAGGAGCATGATGGTGGTGGACCGAAGCTTACATTCACAGCACT 1310
QY 432 LeuLeuSerSerGlnAlaGlnSerLeuThr-----LeuLeuThrThr 445
Db 1311 CTC-----CTCAGCGCACAAAAGCTGACTGATGATCAGGGCCCCGCTCTGATGACCAT 1364
QY 446 ValAlaMetProValPheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGly 465
Db 1365 GTAGCCATGCCTGTGTGTAGTAAGCAGAACGAAACAGATCGAAGGGCATTCCTCTGGGA 1424
QY 466 ValValGlySerAspValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeu 485
Db 1425 GTGGTTGGCACAGATGTCCAGTGAAAGAACTTCTGAAGACCATCCCAAAATACAAAGTTA 1484
QY 486 GlyValHisGlyTyrAlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAsp 505
Db 1485 GGGATTCACGGTTATGCCTTTCGAATACAAATAATGGATATATCTCGCAGCATCCGGAA 1544
QY 506 LeuArgProLeuTyrArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerVal 525
Db 1545 CTCAGGCTGCTGTACGAAGAAGAAAAAG---CGAAGGAAACCTTAACCTATAGTAGCGTT 1601
QY 526 AspLeuSerGluValGluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsn 545
Db 1602 GACCTCTCTGAGGTGGAGTGGGAAGACCAGATGACGCTTGAGAAATGCTATGGTGAAT 1661
QY 546 ArgGluThrGlyThrLeuSerMetAspValLysValProMetAspLysGlyLysArgVal 565
Db 1662 CGAAAGCGGGGAAGTTCATGGAGGTGAAGAGACAGATGGAGCAAAAGGAAACGGGTT 1721
QY 566 LeuPheLeuThrAsnAspTyrPheThrAspIleSerAspThrProPheSerLeuGly 585
Db 1722 TTGGTGATGACAAATGACTACTATTATACAGACATCAAGGGTACTCTCTTTCAGTTAGGT 1781
QY 586 AlaValLeuSerArgGlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGlu 605

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Db 1782 GTGGCGCTTTCCAGAGTCCATGGGAAATATTTCTTCGAGGGGAATGTAAACCATCGAAGAA 1841
Qy 606 GlyLeuHisAspLeuLeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIle 625
Db 1842 GGCCTGCATGACTTAGAACATCCGATGTGCTTCCTGGCAGATGATGGTCTACTGCAAC 1901
Qy 626 ThrAspIleAspProAspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeu 645
Db 1902 ACTGACCTACACCTGAGCACCAGCCATCTGTCTCAGTTAGAGCGATTAAAGCTCTACCTA 1961
Qy 646 ThrArgLysAspProAspLeuGluCysAspGluLeuValArgGluValLeuPheAsp 665
Db 1962 AAGGCAAGAACCTCTGCTCCAGGTGTGATAAGAAATGATCAAGAAGTCCCTTTTTCAC 2021
Qy 666 AlaValValThrAlaProMetGluAlaTyrTrpThrAlaLeuAlaLeuAseMetSerGlu 685
Db 2022 GCGTGTGTGAGTGCCGCCCATTTGAAGCGTATTGGACACAGCTGGCCCTCAACAAATCTGAA 2081
Qy 686 GluSerGluHisValValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSer 705
Db 2082 AATTCTGACAAAGGCGTGGAGTTGCTCTCTCGGCACCTCGCACGGCCCTCTCCAGATC 2141
Qy 706 SerLeuPheValGlySerGluLysValSerAspArgLysPheLeuThrProGluAspGlu 725
Db 2142 AACCTGTTTGTGGGGCTGAGCAGCTCACCAATCAGGACTTCCTGAAAGCTGGTGCAAG 2201
Qy 726 AlaSerValPheThrLeuAspArgPheProLeuTrpTyrArgGlnAlaSerGluHisPro 745
Db 2202 GAGNACATTTTAACGCAGACCATTTCCCTCTCTGTTACCGAAGCGCGTGAGCAGATT 2261
Qy 746 AlaGlySerPheValPheAsnLeuArgTrpAlaGluGlyProGluSerAlaGlyGluPro 765
Db 2262 CCAGGAGCTGCTGCTACTCGATCCCATTCAGCACTGGACCA-----GTCAATAAAGC 2315
Qy 766 MetValValThrAlaSerThrAlaValAlaValThrValAspLysArgThrAlaIleAla 785
Db 2316 AATGTGTGTGACAGCAAGTATCATCTCAGCTCTGGATGAACGGAATCTCTGTGGTG 2375
Qy 786 AlaAlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThr 805
Db 2376 GCAGCTGTAGGCATTCAGATGAACTTGAATTTTCCAAAGGAATTCGGACTGCCAGC 2435
Qy 806 ArgGlnCysSerThrValAspGlyProTyrTrpGlnSerCysGluAspSerAspLeuAsp 825
Db 2436 AGACAGTGTGCTTCCCTCGATGGCAATGTCTCCATCAGCTGTGTGATGATGAGACTGTGAAT 2495
Qy 826 CysPheValIleAspAsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGly 845
Db 2496 TGTACCTCTAGACAATAATGGATTTATTTTGTGTCTGAAGACTACACACAGACTGGA 2555
Qy 846 ArgPheLeuGlyGluValAspGlyValAlaValLeuThrGlnLeuLeuSerMetGlyValPhe 865
Db 2556 GACTTTTGTGTGATGATGAGGAGCTGTGATGAACAAATTTGCTAACAATGGGCTCCTTT 2615
Qy 866 SerGlnValThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisSer 885
Db 2616 AAAAGAAATTACCTTTATGACTACCAAGCCATGTGTAGAGCCAAACAAGGAAGCAGCGAT 2675
Qy 886 AlaAlaGlnProLeuValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeu 905
Db 2676 GGCCCCCATGCTCTGGATCCTTATATAGCTTCTCTCTGAGTAATAATGATCATG 2735
Qy 906 GlnGluLeuValLeuPheLeuGluTrpSerValTrpGlySerTrpTyrAspArgGly 925
Db 2736 ACAGAACTTGTCTTGTCTCTGGTGAATTTAACTCTGC---AGTTGGTGCACCTCCGAT 2792
Qy 926 AlaGluAlaLysSerValPheHisHisSerHisLysLysGlnAspProLeuGln 945
Db 2793 ATGACAGCTAAAGCC-----CAGAAATTTGAACACAGCCCTGGAG 2831
Qy 946 ProCysAspThrGluTyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGly 965
Db 2832 CCTTGTGATCTAGTAATATCCAGCAATTGCTCTCTGAGCGCCACCATCAAGGAGACTACAGGG 2891
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Qy 966 IleValGluCysGlyProCysGlnLysValPheValValGlnGlnIleProAsnSerAsn 985
Db 2892 AATATTGCTGTGAGAGACTGCTCCAAGTCTCTTTGTATCCAGCAAAATCCCAAGCAGCAAC 2951
Qy 986 LeuLeuLeuLeuValThrAspProThrCysAspCysSerIlePheProProValLeuGln 1005
Db 2952 CTGTTTCATGTGTGTGGTGACAGCAGCTGCTCTCTGTAATCTGTGGCCCCCATCCCATG 3011
Qy 1006 GluAlaThrGluValLysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLys 1025
Db 3012 GCACCCATTGAAATCAGGTATATGAATCCCTTAAGTGTGAACGTCTAAAGGCCCAGAG 3071
Qy 1026 LeuArgArgArgProAspSerCysHisAlaPheHisProGluValArgValGluAlaAsp 1045
Db 3072 ATCAGAAGGCCGCCAGAAATCTTGTTCATGGCTTCATCTCTGAG-----GAGAATGCAAGG 3125
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Db 3126 GAGTG-TGGGGGTGCGCCGAGTCTTCCAAGCCCA 3157

RESULT 10
US-09-875-423-3
; Sequence 3, Application US/09875423
; Patent No. US20020081657A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: 21784, A NOVEL HUMAN CALCIUM CHANNEL
; FILE REFERENCE: 10448-059001
; CURRENT APPLICATION NUMBER: US/09/875,423
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3276
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-875-423-3

Alignment Scores:
Pred. No.: 0 Length: 3276
Score: 3416.50 Matches: 628
Percent Similarity: 77.81% Conservative: 189
Best Local Similarity: 59.81% Mismatches: 212
Query Match: 59.67% Indels: 22
DB: 7 Gaps: 7

US-09-833-222A-10 (1-1090) x US-09-875-423-3 (1-3276)
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Qy 33 GlySerLeuLeuLeuGlnLysTyrLysAspValGluSerSerLysLysIleGluGlu 52
Db 184 GGTTCGCCAGCTTCTGCAAAAGAAATACAAAGAGTATGAGAAAGACGTTGCCATAGAAGAA 243
Qy 53 ValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArgArg 72
Db 244 ATTGATGGCTTCCAACTGGTAAAGAGCTGGCAAGAACATGGGAAGAGATGTTTCACAG 303
Qy 73 LysValGluAlaValGlnAsnLeuValGluAlaAlaGluAlaAspLeuAsnHisGlu 92
Db 304 AGTCTGAGGCCGCTCAGGCGCTCTGGTGGAGGCTGCAGAGAAGCACACCTGAAACATGAA 363
Qy 93 PheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArgAspGlu 112
Db 364 TTTGATGCAGACTTACAGTATGAATCTTCAATCTGTGCTGATAAATGAAGGGGACAA 423
Qy 113 LysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHisPheSer 132
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Db 424 GACGGGAATTTTGGAGCTGGGAAGGAATTCATCTTAGCCCCCAATATGACCAATTTAAT 483
QY 133 AsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyrAsnLys 152
Db 484 AATTTGCTGTGAACATCAGTCTAAGTGAGCTCCAAAGTACCAACGAACTGTACAACAA 543
QY 153 AspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPheValGlu 172
Db 544 GACCTGCAATTTGCAATGGGTTTATGGTCTGAAATCTCTAAACAAAGTTTTGTAGAT 603
QY 173 AsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhePhe 192
Db 604 AACTTTGACCGTGACCCATCTCTCATATGCGAGTACTTTTGGAAAGTGCAAAGGGCTTTTT 663
QY 193 ArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPheAspCys 212
Db 664 AGCAGTATCCGGGGATTAATGGGAACCAAGATGAGAATGGAGTCATTTGCTTTCGACTGC 723
QY 213 ArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIleLeuVal 232
Db 724 AGNACCGAAATATGGTATATCCAGGACGAACTTCTCCGAAAGACGTGGTCATTTTAGIT 783
QY 233 AspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThrThr 252
Db 784 GACGTCAGTGGCAGCATGAAGGACTCCGTCTGACTATCGGAAGCAACAGTCTCATCC 843
QY 253 IleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAspTyrVal 272
Db 844 ATTTTGGATACATCTGGGATGATGACTCTTCAACATAATTCCTTATATAGGAGCTT 903
QY 273 HisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsnArgGlu 292
Db 904 CACTATGTGGAACCTTGCCGTGAATGGAACTTTGCCCAAGGAATTTGGAATTTGGATATAGCT 1023
QY 293 HisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValValAspGlnAla 312
Db 964 CACTTCAGGGAGCATCTGGACAAACTTTCCCAAGGAATTTTCAACCCACCGGGCAAGGAATATCTGC 1083
QY 313 LeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySerLeuCys 332
Db 1024 CTGAATGAGGCCCTTCAACATCTCGAGTGAATTTTCAACCCACCGGGCAAGGAATATCTGC 1083
QY 333 AsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProValPheGlu 352
Db 1084 AGTCAGGCCATCATGTCTAATCATGATGGGCGGTGGACACCTATGATACAACTTTTGCA 1143
QY 353 LysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArgGluVal 372
Db 1144 AATACAAATTTGGCAGATCGAAAGGTTGCGATCTTCACATACCTCATTTGGACGAGAGGCT 1203
QY 373 SerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrGlnIle 392
Db 1204 GCCTTTGCAGACAATCTTAAGTGGATGGGCTGTCACCAACAAAGGATTTTTTACCCAGATC 1263
QY 393 SerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSerArgPro 412
Db 1264 TCCACCTTGCTGATGTGCAGGAGATGTCATCGAATACCTTCACGTGCTTAGCCGGCCC 1323
QY 413 MetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSerLysLeu 432
Db 1324 AAAGTCATCGACGAGCATGATGGTGTGGACCGAAGCTTACATTTGACAGCACTCTC 1383
QY 433 LeuSerSerGlnAlaGlnSerLeuThr-----LeuLeuThrVal 446
Db 1384 -----CCTCAGGCACAAAGCTGACTGATGATCAGGGCCCCCTCTGATGACCACTGTA 1437
QY 447 AlaMetProValPheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyVal 466
Db 1438 GCCATGCCGTGTTAGTAAGCAGACAGCAACCAACAGATCGAAGGGCATTTCTTCTGGGAGTG 1497
QY 467 ValGlySerAspValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGly 486

Db 1498 GTTGGCACAGATGTCCCGAGTGAAAGAACTTCTGAAGACCATCCCAAAATACAAGTTAGGG 1557
QY 487 ValHisGlyTyrAlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeu 506
Db 1558 ATTCAACGGTTATGCGCTTTCCTCAATAATCGAAATAATGGATATATCTGACGATCCGGAATC 1617
QY 507 ArgProLeuTyrArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAsp 526
Db 1618 AGGCTGCTGTACGAAGAGGAAAAAG---CGAAGGAAACCTTAACATATAGTAGCGTTGAC 1674
QY 527 LeuSerGluValGluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArg 546
Db 1675 CTCTCTGAGTGGAGTGGGAAGACCGAGATGACGTGTCAGAAATGCTATGGTGAATCGA 1734
QY 547 GluThrGlyThrLeuSerMetAspValLysValProMetAspLysGlyLysArgValLeu 566
Db 1735 AAGACGGGGAAGTTTTTCATGGAGGTGAAGAAAGACAGTGGCAAGGGAACCGGGTTTG 1794
QY 567 PheLeuThrAsnAspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAla 586
Db 1795 GTGATGACAAATGACTACTATTATACAGACATCAAGGTACTCTCTTCAGTTTAGGTGTG 1854
QY 587 ValLeuSerArgGlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGly 606
Db 1855 GCGCTTTCCAGAGGTTCATGGAAATATTTCTTCCGAGGGAATGTAACCATCGAAGAAGGC 1914
QY 607 LeuHisAspLeuLeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThr 626
Db 1915 CTGCAATGACTTAAACATCCCGATGTCTTGGCAGATGAATGGTCTTACTGCAACACT 1974
QY 627 AspIleAspProAspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThr 646
Db 1975 GACCTACACCTTGAGCACCCTCATCTGTCTCAGTTAGAACGATTAAGCTCTACCTAAAA 2034
QY 647 ArgLysAspProAspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAla 666
Db 2035 GGCAAAAGAACCTCTGCTCCAGTGTGATAAGAAATTGATCCAAGAACTCTCTTTTGACGC 2094
QY 667 ValValThrAlaProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGlu 686
Db 2095 GTGGTGAGTGCCCCCATTTGAAGCGTATTGGACGAGCTGGCCCTCAACAAATCTGAAAT 2154
QY 687 SerGluHisValAlaAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSer 706
Db 2155 TCTGACAGGGCGTGAGGTTGCTCTCTCGCAGCTCGCAGCGCTCTCCAGAAATCAAC 2214
QY 707 LeuPheValGlySerGluLysValSerAspArgLysPheLeuThrProGluAspGluAla 726
Db 2215 CTGTTTGTGGGGCTGAGCAGCTCCCAATCAGGACTTCTGAAAGCTGGCGACAGGAG 2274
QY 727 SerValPheThrLeuAspArgPheProLeuTyrTyrArgGlnAlaSerGluHisProAla 746
Db 2275 AACATTTTAAACGACACCATTTCTCTCTGTACCGAAGAGCCGCTGAGCAGATTCCA 2334
QY 747 GlySerPheValPheAsnLeuArgTrpGlnGlyProGluSerAlaGlyGluProMet 766
Db 2335 GGGAGCTTCGTCTACTCGATCCCAATTCAGCACTGGACCA-----GTCAATAAAGCAAT 2388
QY 767 ValValThrAlaSerThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAla 786
Db 2389 GTGGTGACAGCAAGTACATCCATCCAGCTCTCTGGATGAACCGGAAATCTCTCTGTGGTGA 2448
QY 787 AlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaIleThrArg 806
Db 2449 GCTGTAGGCATTCAGATGAATTTGAAATTTTCCAAAGGAAGTTCTTGGACTGCCACAGA 2508
QY 807 GlnCysSerThrValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCys 826
Db 2509 CAGTGTGCTTCCGTGGTGGCAAAATGCTCCATCAGCTGTGATGATGAGACTGTGAATGT 2568
QY 827 PheValIleAspAsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArg 846
Db 2569 TACCTCATAGACAAATAATGGATTTATTTGGTGTCTGAAGACTTACACACAGACTGGAGAC 2628

Qy	173	AenPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhePhe	192
Db	604	AACTTTGACCGTGACCCATCTCTCATATGGCAGTACTTTGGAAGTGCAAGAGGCTTTT	663
Qy	193	ArgIleTyrProGlyVlleTyrThrProAspGluAenGlyValIleThrPheAspCys	212
Db	664	AGGCAGTATCCGGGATTTAAATGGGAACGATGAGATGGAGTCAITTCCTTCGATGTC	723
Qy	213	ArgAenArgGlyTyrTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIleLeuVal	232
Db	724	AGGAACCGAAAAATGGTACATCCAGCAGCAACTTCTCCGAAAGACGGTGCATTTAGTT	783
Qy	233	AspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisIleThrThr	252
Db	784	GACGTGATGGCAGCATGAAGGACTTCGTCTGACTATCGCGAAGCAACAGTCTCATCC	843
Qy	253	IleLeuAspThrLeuGlyGluAenAspPheValAenIleIleAlaTyrAenAspTyrVal	272
Db	844	ATTTTGGATACACTTGGGGATGATGACTTCTTCAACATATGCTTATATGAGAGGCTT	903
Qy	273	HisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsnArgGlu	292
Db	904	CACATATGGGAACCTTGCTCGAATGGAACCTTTGGTGCAGCCGACAGCAACAAAGAG	963
Qy	293	HisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAspGlnAla	312
Db	964	CACATTCAGGGAGCATCTGGACAAACTTTTCCGCCAAGGAATTGGAAATGTGGATATAGCT	1023
Qy	313	LeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySerLeuCys	332
Db	1024	CTGAATGAGGCCTTCAACATTTCTGATGATTTTCAACCACACGGGCACAAGGAAGTATCTGC	1083
Qy	333	AsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProValPheGlu	352
Db	1084	AGTCAGGCCCATCATGCTCTATAACTTGATGGGGCGGTGGACACTATGATCAACAATCTTTGCA	1143
Qy	353	LysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyValArgGluVal	372
Db	1144	AAATACAAATTTGGCCAGATCGAAAGGTTTCGCATCTTTCACATACCTCATTTGGACGAGAGCT	1203
Qy	373	SerPheAlaAspArgMetLysTrpIleAlaCysAenAenLysGlyTyrTyrThrGlnIle	392
Db	1204	CGGTTTGACAGCAATCTAAAGTGATGGCTTGCCCAACAAAGGATTTTTCACCCAGATC	1263
Qy	393	SerThrLeuAlaAspThrGlnGluAenValMetGluTyrLeuHisValLeuSerArgPro	412
Db	1264	TCCACCTTGGCTGATGTGCAGGAGAAATGTCATGGAATACCTTTCAGTGTCTTAGCCGGCC	1323
Qy	413	MetValIleAenHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSerLysLeu	432
Db	1324	AAAGTCAATCGACAGGAGCATGATGTGTGTGGACCGAAGCTTACATTCAGCAGCACCTC	1383
Qy	433	LeuSerSerGlnAlaGlnSerLeuThr-----LeuLeuThrThrVal	446
Db	1384	-----CCTCAGGCACAAAAGCTCAGCTGATGATCAGGGCCCCGCTTCGTGATGCCACCTGTA	1437
Qy	447	AlaMetProValPheSerLysLysAenGluThrArgSerHisGlyIleLeuLeuGlyVal	466
Db	1438	GCCATGCTGTGTTTAGTAGCAGACGAAACCAAGATCGAAGGGCATCTTCTTGGGAGTG	1497
Qy	467	ValGlySerAspValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGly	486
Db	1498	GTTGGCAGAGTGTCCAGGTGAAGAAGACTTCTGAAGACCAATCCCCCAATACAAAGTTAGGG	1557
Qy	487	ValHisGlyTyrAlaPheLeuAenThrAsnAsnGlyTyrIleLeuSerHisProAspLeu	506
Db	1558	ATTCAACGGTTATGCTTTTGCNATCACAATATATGATATATCTCTGACGCATCCGGAATCT	1617
Qy	507	ArgProLeuTyrArgGlyLysLeuLysProLysProAsnTyrAsnSerValAsp	526
Db	1618	AGGCTGCTACGAAGAAGGAAAAAAG---CGAAGGAGAAACCTAACTATAGTAGCGTTGAC	1674

Qy	527	LeuSerGluValGluTyrGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArg	546
Db	1675	CTCTCTGAGGTGGAGTGGGAAGACCGAGATGCGTGTGTGAAATGCTATGGTGAATCGA	1734
Qy	547	GluThrGlyThrLeuSerMetAspValIysValProMetAspIysGlyIysArgValLeu	566
Db	1735	AAGACGGGGAAGTTTTCATGGAGGTGAGAACAGACAGTGGACAAAGGAACGGGTTTG	1794
Qy	567	PheLeuThrAsnAspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAla	586
Db	1795	GTGATGACAAATGACTACTATTATACAGACATCAAGGGTACTCCTTTCACTTAGGTGTG	1854
Qy	587	ValLeuSerArgGlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGly	606
Db	1855	CGCGTTTCCAGAGTCAATGGAAATATTTCTTCGAGGGAATGTAAACATCGAAGAAGGC	1914
Qy	607	LeuHisAspLeuLeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThr	626
Db	1915	CTGCATGACTTAGAACATCCCGATGTGTCTTGGCAGATGAATGGTCTTACTGCAACACT	1974
Qy	627	AspIleAspProAspHisArgIysLeuSerGlnLeuGluAlaMetIleArgPheLeuThr	646
Db	1975	GACCTACACCTCGAGCACCGCCATCTGTCTCAGTTAGAAGCGATTAAAGCTTCTACCTAAA	2034
Qy	647	ArgIysAspProAspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAla	666
Db	2035	GGCAAGAACCTCTGCTCCAGTGTGATTAAGATTGATCCAGAAGTCCCTTTTGACGGC	2094
Qy	667	ValValThrAlaProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGlu	686
Db	2095	GTGTGTAGTGCCTCATTTGAAGCGTATTGGACAGAGCTGGCCCTCAACAAATCTGAAAAT	2154
Qy	687	SerGluHisValValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSer	706
Db	2155	TCTCACAAAGGCGTGGAGGTGTGCTCTCGGCACATCGCACGGGCGCTCTCCAGAATCAAC	2214
Qy	707	LeuPheValGlySerGluLysValSerAspArgLysPheLeuThrProGluAspGluAla	726
Db	2215	CTGTGTTCTGGGGCTGAGCAGCTCACCAATCAGAGCTTCTCGAAAGCTGCGCAACAGGAG	2274
Qy	727	SerValPheThrLeuAspArgPheProLeuTyrTyrArgGlnAlaSerGluHisProAla	746
Db	2275	AACATTTTTTAACGCAGACCAATTTCCCTCTCTGTGATCCGAAGAGCCGCTCGAGCAGATCCA	2334
Qy	747	GlySerPheValPheAsnLeuArgTyrAlaGluGlyProGluSerAlaGlyGluProMet	766
Db	2335	GGGAGCTTCGTCTACTCGATCCCATTCAGACACTGGACCA-----GTCAATAAAGCAAT	2388
Qy	767	ValValThrAlaSerThrAlaValAlaValThrValAspIysArgThrAlaIleAlaAla	786
Db	2389	GTGTGTGACAGCAGTATCATCCATCCAGCTCCTGGATGAACGGAAATCTCCTGTGGTGGCA	2448
Qy	787	AlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArg	806
Db	2449	GCTGTAGCATTCAGATGAACCTTGAATTTTCCAAAGGAAGTTCTGGACTGCCACAGA	2508
Qy	807	GlnCysSerThrValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCys	826
Db	2509	CAGTGTGCTCTCCCTGGATGGCAAAATGCTCCATCAGCTGTGATCAGAGCTGTGAATGTG	2568
Qy	827	PheValIleAspAsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArg	846
Db	2569	TACCTCATGACAAATAATGATTTATTTTGGTGTCTGAAGACTTACACAGACTGGAGAC	2628
Qy	847	PheLeuGlyGluValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSer	866
Db	2629	TTTTTTGTCGATCGAGGAGCTGTGATGAACAAATTCGTAACATGGCTCTTTAAA	2688
Qy	867	GlnValThrMetTyrAspTyrGlnAlaMetCysGlyProSerSerHisHisSerAla	886
Db	2689	AGAAATTACCTTTATGACTACCAAGCGCATGTGTAGAGCCCAAGGAAGACGCGATGGC	2748
Qy	887	AlaGlnProLeuValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGln	906

QY 313 LeuArgGluAlaPheGlnIleLeuLysGlnPheGlnAlaLysGlnGlySerLeuCys 332
DB 1024 CTGAATGAGGCTTCAACATTCCTGAGTGATTTCAACACAGGACAGAGAGATATCTGC 1083
QY 333 AsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProValPheGlu 352
DB 1084 AGTCAGGCCATCATGCTCATAACTGATGGGCGGTGGACACCTATGATACAATCTTTGCA 1143
QY 353 LysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArgGluVal 372
DB 1144 AAATACAAATTTGGCAGATCAAGAGTTCCGATCTTCATACCTCATTTGGACGAGAGCT 1203
QY 373 SerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThrGlnIle 392
DB 1204 GCGTTTGCACACAATCTAAGTGGATGGCTGTGCGCAACAAGAGATTTTTTACCAGATC 1263
QY 393 SerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSerArgPro 412
DB 1264 TCCACCTTGCTGATGTGCAGGAGAATGTCTATGGAATACCTTCACGCTGTAGCCGCC 1323
QY 413 MetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSerLysLeu 432
DB 1324 AAAGTATACAGCAGGACGATGATGGTGTGGACCGAAGCTTACATTTGACACACTCTC 1383
QY 433 LeuSerSerGlnAlaGlnSerLeuThr-----LeuLeuThrThrVal 446
DB 1384 -----CCTCAGGCACAAAAGCTGACTGATGATCAGGCCCCGCTGCTGATGACCACTGTA 1437
QY 447 AlaMetProValPheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyVal 466
DB 1438 GCCATGCTGTGTAGTAGCAGAGAAGCAACAGATCGAAGGCGCATCTCTCTGGGAGTG 1497
QY 467 ValGlySerAspValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGly 486
DB 1498 GTTGGCAGATGCTCCAGTGAAGAACTCTCGAAGACCATCCCAACATAAAGTAGTAGG 1557
QY 487 ValHisGlyTyrAlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeu 506
DB 1558 ATTACCGTTATGCTTTGCAATCACAAATAATGGATATATCTGACGCATCCGGAATC 1617
QY 507 ArgProLeuTyrArgGluGlyLysLysLeuLysPheProLysProAsnTyrAsnSerValAsp 526
DB 1618 AGCGCTGTGTACGAAGAAGGAAAAAG--CGAAGGAAACCTAACTATATAGTAGCTTGAC 1674
QY 527 LeuSerGluValGluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArg 546
DB 1675 CTCTCGAGGTGAGTGGGAAGACCGAGATGCTGTGAGAAATGCTATGGTAATCGA 1734
QY 547 GluThrGlyThrLeuSerMetAspValLysValProMetAspLysGlyLysArgValLeu 566
DB 1735 AAGACGGGAAGTTTTCCATGGAGGTGAAGAAGACAGACAGTGCACAAAGGAAACGGGTTTG 1794
QY 567 PheLeuThrAsnAspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAla 586
DB 1795 GTGATGACAAATGACTACTATTATACAGACATCAAGGGTACTCTTCATGTTTAGGTGTG 1854
QY 587 ValLeuSerArgGlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGly 606
DB 1855 GCGCTTTCNAGAGTCAATGGGAATATTTCTCCGAGGGGAATGTAAACATCGAAGAAGC 1914
QY 607 LeuHisAspLeuLeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThr 626
DB 1915 CTGCATGACTTAGAACATCCGATGTGCTCTGGCAGATGAATGGTCTTACTGCAACACT 1974
QY 627 AspIleAspProAspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThr 646
DB 1975 GACCTACACCTGAGCAGCCGCAATCTGCTCTCAGTTAGAAGCGGATTAAGCTCTACCTAAAA 2034
QY 647 ArgLysAspProAspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAla 666
DB 2035 GGCAAAGAACCTCTGCTCCAGTGTGATAAAGAAATGATCCAGAAGTCTCTTTTGACGG 2094
QY 667 ValValThrAlaProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGlu 686

DB 2095 GTGGTGAGTGCCTCCCATTCGAAGCGTATTGGACCGCTGGCCCTCAACAAATCTGAAAT 2154
QY 687 SerGluHisValValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSer 706
DB 2155 TCTGACAAGGGGTGGAGGTGCTTCTCTCGGCACCTCGCACGGGCTCTCCAGAATCAAC 2214
QY 707 LeuPheValGlySerGluLysValSerAspArgLysPheLeuThrProGluLeuAspGluAla 726
DB 2215 CTGTTTGTGGGGCTGAGCAGCTCACCAATCAGGACTTCTGAAAGCTGGCGACAGGAG 2274
QY 727 SerValPheThrLeuAspArgPheProLeuTyrTyrArgGlnAlaSerGluHisProAla 746
DB 2275 AACATTTTAAACGACAGACCATTTCCCTCTCTGTACCGAAGAGCGCTGAGCAGATTCCA 2334
QY 747 GlySerPheValPheAsnLeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMet 766
DB 2335 GGGAGCTTCTCTACTCTGATCCCATTTCCAGACTGGACCA-----GTCAATAAAGCAAT 2388
QY 767 ValValThrAlaSerThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAla 786
DB 2389 GTGGTGACAGCAAGTACATCCATCCAGCTCTCTGGATGAACGGAATCTCTCTGTGGCA 2448
QY 787 AlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArg 806
DB 2449 GCTGTAGGCATTCAGATGAAACTTGAATTTTCCAAAGGAAGTTCTGGACTGCCAGAGA 2508
QY 807 GlnCysSerThrValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCys 826
DB 2509 CAGTGTGCTCTCTGGATGGCAATGCTCCATCAGCTGTGATGATGAGACTGTGAATTGT 2568
QY 827 PheValIleAspAsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArg 846
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QY 847 PheLeuGlyGluValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSer 866
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QY 867 GlnValThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisSerAla 886
DB 2689 AGAATTACCTTTATGACTACCAAGCCATGTGTAGAGCCCAACAAAGAAAGCAGCGATGC 2748
QY 887 AlaGlnProLeuValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuGln 906
DB 2749 GCCATGGCTCTCTGGATCCTTATATGCTCTCTCTGACGATAAAATGGATCATGACA 2808
QY 907 GluLeuValLeuPheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAla 926
DB 2809 GAACTTGTCTTCTCTGTGGAAATTAACCTCTGC---AGTTGGTGCACTCCGATATG 2865
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QY 967 ValGluCysGlyProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLeu 986
DB 2965 ATTGTGTGGAAGACTGTCTCAAGTCTTGTTCATCCAGCAAAATCCCAAGCAGCAACCTG 3024
QY 987 LeuLeuLeuValThrAspProThrCysAspCysSerIlePheProProValLeuGlnGlu 1006
DB 3025 TTCATGGTGGTGAGCAGAGCTGCTCTCTGTAATCTGTGCCCCCATCACCATGGCA 3084
QY 1007 AlaThrGluValLysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeu 1026
DB 3085 CCCATTGAAATCAGGTATAATGAATCCCTTAAGTGTGAACGCTTAAAGCCCCCAGAGATC 3144
QY 1027 ArgArgArgProAspSerCysHisAlaPheHisProGluValArgValGluAlaAspArg 1046

Db 1703 CTCTCTGAGTGGAGTGGGAGACCGAGATGACGTGTGGAGAAATGCTATGGTGAATCGA 1762
Qy 547 GluThrGlyThrLeuSerMetAspValLysValProMetAspLysGlyLysArgValLeu 566
Db 1763 AAGACGGGAGTTCCTTCCATGGAGGTGAAGACAGACAGTGGACAAAGGAAACGGGTTTG 1822
Qy 567 PheLeuThrAsnAspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAla 586
Db 1823 GTGATGACAAATGACTACTATTATACAGACATCAAGGGTACTCTTTCAGTTTAGTGTG 1882
Qy 587 ValLeuSerArgGlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGly 606
Db 1883 GCGCTTTCCAGAGTTCATCGGAATATTTCTCCGAGGAATGTAAACCATCGAAGAAGGC 1942
Qy 607 LeuHisAspLeuLeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThr 626
Db 1943 CTGCATGACTTAGAACATCCGAGTGTCTCTGGCAGATGAATGGTCCCTACTCGCAACACT 2002
Qy 627 AspIleAspProAspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThr 646
Db 2003 GACCTACACCTGAGCACCCTCATCTCTCAGTTAGAGCGATTAAAGCTCTACCTTAAA 2062
Qy 647 ArgLysAspProAspLeuGluCysAspGluGluValArgGluValLeuPheAspAla 666
Db 2063 GGCAAAAGAACCTCTGCTCCAGTGTGATAAAGAAATTGATCCAAAGAGTCTTTTTCACGG 2122
Qy 667 ValValThrAlaProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGlu 686
Db 2123 GTGGTGAGTCCCCCATTAAGCGATTTGGACAGCTGTGCCCTCAACAAATCTGAAAT 2182
Qy 687 SerGluHisValValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSer 706
Db 2183 TCTGACAAAGGCGTGGAGGTGCTCTCTCGGCACTCGCAGGGCTCTCCAGAAATCAAC 2242
Qy 707 LeuPheValGlySerGluLysValSerAspArgLysPheLeuThrProGluAspGluAla 726
Db 2243 CTGTTTGTGCGGGCTGAGCAGCTCACCAATCAGGACTTCTCGAAAGCTGGCGACAAGGAG 2302
Qy 727 SerValPheThrLeuAspArgPheProLeuTyrTrpArgGlnAlaSerGluHisProAla 746
Db 2303 AACATTTTAAACCACAGCACTTTCCCTCTCTGTGTACGGAAGACCCCTGAGCAGATCCA 2362
Qy 747 GlySerPheValPheAsnLeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMet 766
Db 2363 GGGAGCTTCTCTACTCGATCCCATTCAGCAGCTGGACCA-----GTCAATAAAGCAAT 2416
Qy 767 ValValThrAlaSerThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAla 786
Db 2417 GTGGTGACAGCAAGTACATCCATCCAGCTCCCTGGATGAACGGAAATCTCTGTGTGGCA 2476
Qy 787 AlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLysPheThrAlaAlaThrArg 806
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Qy 807 GlnCysSerThrValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCys 826
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Qy 827 PheValIleAspAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArg 846
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Qy 847 PheLeuGlyValAspGlyAlaValLeuThrGlnLeuSerMetGlyValPheSer 866
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Qy 867 GlnValThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisSerAla 886
Db 2717 AGAATTAACCTTTATGACTACCAAGCAATGTGTAGAGCCAAACAGAAAGCAGCGATGC 2776
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Qy 927 GluAlaLysSerValPheHisHisSerHisLysHisLysLysGlnAspProLeuGlnPro 946
Db 2894 ACAGCTAAAGCC-----CAGAAATTGAACACAGACCCTGGAGCCT 2932
Qy 947 CysAspThrGluTyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIle 966
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Qy 1007 AlaThrGluValLysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeu 1026
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RESULT 14
US-10-162-012-14
; Sequence 14, Application US/10162012
; Publication No. US20030051660A1
; GENERAL INFORMATION:
; APPLICANT: Curtiss, Rory A. J.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
; FILE REFERENCE: 10448-190001
; CURRENT APPLICATION NUMBER: US/10/162,012
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/209,845
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: US 09/875,321
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: PCT/US01/18340
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,423
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18398
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,238
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; PRIOR APPLICATION NUMBER: PCT/US01/18247
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/227,068
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; PRIOR APPLICATION NUMBER: US 09/928,530
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; PRIOR FILING DATE: 2001-08-21

; PRIOR APPLICATION NUMBER: PCT/US01/26096
 ; PRIOR FILING DATE: 2001-08-21
 ; PRIOR APPLICATION NUMBER: US 60/279,281
 ; PRIOR FILING DATE: 2001-03-28
 ; PRIOR APPLICATION NUMBER: US 10/109,029
 ; PRIOR FILING DATE: 2002-03-28
 ; PRIOR APPLICATION NUMBER: PCT/US02/09728
 ; PRIOR FILING DATE: 2002-03-28
 ; PRIOR APPLICATION NUMBER: US 60/290,288
 ; PRIOR FILING DATE: 2001-05-11
 ; PRIOR APPLICATION NUMBER: US (not assigned)
 ; PRIOR FILING DATE: 2002-05-13
 ; NUMBER OF SEQ ID NOS: 48
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 14
 ; LENGTH: 3690
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (29)...(3301)
 ; US-10-162-012-14

Alignment Scores:
 Pred. No.: 0 Length: 3690
 Score: 3416.50 Matches: 628
 Percent Similarity: 77.81% Conservative: 189
 Best Local Similarity: 59.81% Mismatches: 212
 Query Match: 59.67% Indels: 22
 DB: 15 Gaps: 7

US-09-833-222A-10 (1-1090) x US-10-162-012-14 (1-3690)

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Db	152	GTGAAGCTCTGGGCTCGGCTTTGGTGGGAGATAAAATCCATTGCTGCTAGTACTCC	211
Qy	33	GlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysLysGluGlu	52
Db	212	GGTTCCAGCTTCTGCAAAAGAAATACAAAGATATGAGAAAGACGTTGCCATAGAAGAA	271
Qy	53	ValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArgArg	72
Db	272	ATTGATGGCTCCAACTGGTAAAGAGCTGGCAAGAACATGGAAGAGATGTTTCAACAG	331
Qy	73	LysValGluAlaValGlnAsnLeuValGluAlaGluAlaAspLeuAsnHisGlu	92
Db	332	AAGTCTGAGGCCGCTCAGGCGCTCTGGTGGAGCTGCAGAAAGACACACTGAAACATGAA	391
Qy	93	PheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuLeuLeuAsnGluArgAspGlu	112
Db	392	TTTGATGCAGACTTACAGTATGAATATCTCAATGCTGTGCTGATATAATGAAAGGGACAA	451
Qy	113	LysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuLeuGluSerAsnAlaHisPheSer	132
Db	452	GACGGGAATTTTGGAGCTGGGAAGAGAAATTCATCTTACCCCAAAATGACCAATTTAAT	511
Qy	133	AsnLeuProValAsnThrSerLysSerValGlnLeuProThrAsnValTyrAsnLys	152
Db	512	AAATTGGCTGTGAACATCAGTCTAAGTGAGCTCCAGTACCAAGAACATGATGACACAAA	571
Qy	153	AspProAspLeuLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPheValGlu	172
Db	572	GACCTTGCATTTGCAATGGGTTTATTGGTCTGAAATCTCTAAACAAAGTTTGTAGAT	631
Qy	173	AsnPheGlnArgAspProThrLeuThrTyrPheGlySerAlaThrGlyPhePhe	192
Db	632	AACCTTTGACCGTACCCCATCTCATATGACGACTTTTGGAGTGCAAAGGGCTTTTT	691
Qy	193	ArgIleTyrProGlyLysLysTyrThrProAspGluAsnGlyValIleThrPheAspCys	212
Db	692	AGCAGTATCCGGGGATTAAATGGGAACCAAGATGAGNATGGAGTCTTGCCTTCGACTGC	751

Qy	213	ArgAsnArgGlyTyrTyrIleGlnAlaAlaThrSerProLysAspIleValIleLeuVal	232
Db	752	AGGAACCGAAAAATGGTACATCCAGGAGCAACTTCTCCGAAGACAGTGGTCAATTTAGTT	811
Qy	233	AspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThrThr	252
Db	812	GACGTAGTGGCAGCATGAAGGACTCCGTCTAGCTATCCGGAAGCAACAGTCTCATCC	871
Qy	253	IleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAspTyrVal	272
Db	872	ATTTTGGATACACTTGGGATGATGACTTCTTCAACATAATTTGCTTATATAGGAGGCTT	931
Qy	273	HisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAsnArgGlu	292
Db	932	CACATATGTGAACCTTTCCTGGAATGGAACTTGGTGCAGCCGACAGCAACAAAGAG	991
Qy	293	HisPheLysLeuLeuValGluLeuMetValLysGlyValGlyValValValAspGlnAla	312
Db	992	CACCTTCAAGGAGCATCTGGACAACTTTTCGCCAAAGAAATTTGGAATTTGGATATAGCT	1051
Qy	313	LeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGlnAlaLysGlnGlySerLeuCys	332
Db	1052	CTGAATGAGGCTTCAACATTTCTGAGTGATTTTCAACCCACAGGAGCAAGGATATCTGC	1111
Qy	333	AsnGlnAlaIleMetLeuLeuSerAspGlyAlaValGluAspTyrGluProValPheGlu	352
Db	1112	AGTCAGGCCATCATGCTCACTAATGATGGGCGGTGGACACCTATGATACAACTTTTGCA	1171
Qy	353	LysTyrAsnTyrProAspCysLysValArgValPheThrTyrLeuIleGlyArgGluVal	372
Db	1172	AAATCAATTTGGCCAGATCGAAAGGTTGCGATCTTCACTACCTCATTTGACGAGAGCT	1231
Qy	373	SerPheAlaAspArgMetLysTyrIleAlaCysAsnAsnLysGlyTyrTyrThrGlnIle	392
Db	1232	CGCTTTTCAGACAACTTAAAGTGGATGGCTGTGCCAACAAAGGATTTTATCCAGATC	1291
Qy	393	SerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSerArgPro	412
Db	1292	TCCACCTTGGCTGATGTCAGGAGAAATGTCATGGAATACCTTCACGTCGCTTAGCGGCC	1351
Qy	413	MetValIleAsnHisAspHisAspIleIleTyrThrGluAlaTyrMetAspSerLysLeu	432
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Qy	467	ValGlySerAspValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGly	486
Db	1526	GTTGGCAGCAGATGTCCTCAGTGAAGAACTTCTGAAGACCATCCCAATAACAATTAGGG	1585
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Qy	527	LeuSerGluValGluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArg	546
Db	1703	CTCTCTGAGGTGGAGTGGGAAGACCGAGATGACGCTTTGAGAAATGCTATGGTGAATCGA	1762
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Db	1763	AAGACGGGGAAGTTTTTCCATGGAGGTGAAGAAGACAGTGGCAAGGAAACGGGTTTTG	1822
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Db 1883 GCGCTTTCCAGAGGTCAATGGGAATATTTCTCCGAGGGAATGTAAACCTCGAAGAAGGC 1942
Qy 607 LeuHisAspLeuLeuHisProAspLeuAlaGlyAspTrpIleTyrcysIleThr 626
Db 1943 CTGCATGACTTAGACATCCGATGTCTCTGGCAGATGAATGGTCTCTACTGCAACACT 2002
Qy 627 AspIleAspProAspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThr 646
Db 2003 GACCTACACCTGAGCACCCTCATCTCTCAGTTAGAGCATTAAGCTCTACCTAAAA 2062
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Db 2063 GGCAAGAAGCCTCTGCTCCAGTGTGATAAGAATTGATCCAAAGAGTCCTTTTGGACGG 2122
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Qy 767 ValValThrAlaSerThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAla 786
Db 2417 GTGGTGACACAGTAGTACATCCATCCAGCTCCTGGATGACGGAATCTCTCTGGTGGGCA 2476
Qy 787 AlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArg 806
Db 2477 GCTGTAGGCATTGAGTGAATTTGATTTTCCAAAGGAAGTTCTGGACTGCCACGAGA 2536
Qy 807 GlnCysSerThrValAspGlyProTyrrThrGlnSerCysGluAspSerAspLeuAspCys 826
Db 2537 CAGTGTGCTTCCCTGGATGGCAAAATGCTCCATCAGCTGTGATGAGACTGTGAATTTGT 2596
Qy 827 PheValIleAspAsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArg 846
Db 2597 TACCTCATAGACAATAATGATTTATTTGGTGTCTGAAAGACTTACACAGACTGGAGAC 2656
Qy 847 PheLeuGlyGluValAspGlyAlaValLeuThrGlnLeuSerMetGlyValPheSer 866
Db 2657 TTTTGTGGTGGATCGAGGAGGTGTGATGAACAAATGCTAACATGGCTCCTTTAA 2716
Qy 867 GlnValThrMetTyrrAspTyrrGlnAlaMetCysGlyProSerSerHisHisSerAla 886
Db 2717 AGAATTACCTTTATGACTACCAAGCATGTGTAGAGCCCAACCAAGAAAGCAGCGATGGC 2776
Qy 887 AlaGlnProLeuValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuGln 906
Db 2777 GCCCATGGCTCTCGATCCTTATAATGCTCTCTCTGCAGTAAAAATGGATCATGACA 2836
Qy 907 GluLeuValLeuPheLeuGluTyrrPsrValTrpGlySerTrpTyrrAspArgGlyAla 926
Db 2837 GAACCTGTCTGTCTCTGGTGGGAATTAACCTCTGC---AGTTGGTGGCACTCCGATATG 2893
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Qy 947 CysAspThrGluTyrrProValPheValTyrrGlnProAlaIleArgGluAlaAsnGlyIle 966
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Db 2993 ATTGCTTGTGAGACTGCTCCAAGTCTTGTGTCATCAGCAATCCNAGCAGCAACCTG 3052
Qy 987 LeuLeuLeuValThrAspProThrCysAspCysSerIlePheProValLeuGlnGlu 1006
Db 3053 TTCACTGGTGTGTGACAGACGCTGCTCTGTGAATCTGTGATCTGTGCCCCCATCCATGGCA 3112
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Db 3113 CCCATTGAATCAGGTATTAATGAATCCCTTAAGTGTGAACGCTTAAAGGCCCAAGATC 3172
Qy 1027 ArgArgArgProAspSerCysHisAlaPheHisProGluValArgValGluAlaAspArg 1046
Db 3173 AGAAGCGGCCAGAAATCTTGTCTATGGCTTCCATCTCTGAG-----CAGAAATGCAAGGAG 3226
Qy 1047 GlyTrpAlaGlyPheSerSerProAsnPro 1056
Db 3227 TG-TGGGGTGGCGCGAGTCTCCAAGCCCA 3255
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; Publication No. US2003023236A1
; GENERAL INFORMATION:
; APPLICANT: Curtiss, Rory A.J.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
; FILE REFERENCE: 10448-190001
; CURRENT APPLICATION NUMBER: US/10/162,102
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/209,845
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: US 09/875,321
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: PCT/US01/18340
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,423
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18398
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,238
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,363
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18247
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/227,068
; PRIOR FILING DATE: 2000-08-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 48
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29) ... (3301)
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Alignment Scores: 0 Length: 3690
Pred. No.: 3416.50 Matches: 628

Percent Similarity:	77.81%	Conservative:	189
Best Local Similarity:	59.81%	Mismatches:	212
Query Match:	59.67%	Indels:	22
DB:	18	Gaps:	7

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Qy	33	GlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIleGluGlu	52
Db	212	GGTTCCAGCTTCTGCAAAAGAAATACAAAGATGATGAGAAAGACGTTGCCATAGAAGAA	271
Qy	53	ValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArgArg	72
Db	272	ATTGATGGCTCCNACTGGTAAGAGCTGGCAAGAACATGGAGAGATGTTTTCACAG	331
Qy	73	LysValGluAlaValGlnAsnLeuValGluAlaGluAlaAspLeuAsnHisGlu	92
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Db	572	GACCCCTGCAATTTGCAATGGGTTTATTGGTCTGTAATCTCTAAACAAAGTTTGTAGAT	631
Qy	173	AsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhePhe	192
Db	632	AACITTTGACGTGACCATCTCTCATATGGCAGTACTTTGGAGTGCAGAGGGCTTTT	691
Qy	193	ArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPheAspCys	212
Db	692	AGGCAGTATCCGGGGATTAAATGGGAACACAGATGAGAAATGGAGTCAATTCGCTTC	751
Qy	213	ArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIleLeuVal	232
Db	752	AGGAACCGAAATGGTACATCCAGGCAGCAACTTCTCCGAAAGACGTGGTCAATTTAGTT	811
Qy	233	AspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThrThr	252
Db	812	GACGTAGTGGCAGACATGAAGAGACTCCGTCTGACTATCCGAAAGCAACAGTCTCATCC	871
Qy	253	IleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAspTyrVal	272
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Qy	273	HisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsnArgGlu	292
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Qy	293	HisPheLysLeuLeuGluLeuMetValLysGlyValGlyValValAspGlnAla	312
Db	992	CACCTTACGGAGCATCTGGACAAACTTTTCCCAAGGAATTTGGATGTTGGATATAGCT	1051
Qy	313	LeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnIleLysLeuCys	332
Db	1052	CTGAATGAGGCTTCAACATTTCTGAGTATTTCAACACACGCGGACAGGAAGTATCTGC	1111
Qy	333	AsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProValPheGlu	352
Db		

Db	1112	AGTCAGGCCCATCATGCTCATAACTGATGGGCGGTGGACACCTATATGATACAATCTTTGCA	1171
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Db	1172	AAATACAAATTTGGCAGATCGAAGGTTCCGATCTTACATACCTCATTTGGACGAGGCT	1231
Qy	373	SerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThrGlnIle	392
Db	1232	GCCTTTGGCAGACAATCTAAAGTGGATGGCTGTGCCAACAAAGGATTTTTTACCAGATC	1291
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Qy	413	MetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSerLysLeu	432
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Qy	433	LeuSerSerGlnAlaGlnSerLeuThr-----LeuLeuThrThrVal	446
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Db	1466	GCCATGCTGTGTTTGTAGTAGCAGAACAAACAGATCGAAGGGCATTTCTTGGGAGTG	1525
Qy	467	ValGlySerAspValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGly	486
Db	1526	GTTTGGCAGCATGCTCCAGTGNAAGAACTTCTGAAGACCATCCCAAAATACAAGTAGGG	1585
Qy	487	ValHisGlyTyrAlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeu	506
Db	1586	ATTTCAGGGTTATGCTTTGCAATCAAAATAATGGATATATCTCTGACGCATCCGGAAC	1645
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Qy	547	GluThrGlyThrLeuSerMetAspValLysValProMetAspLysGlyLysArgValLeu	566
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Qy	607	LeuHisAspLeuLeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThr	626
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Qy	627	AspIleAspProAspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThr	646
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Qy	667	ValValThrAlaProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGlu	686
Db	2123	GTGCTGAGTGGCCCAATTGAAGCGTATGGACCAAGCTGGCCCTCAACAAATCTGAANAAT	2182
Qy	687	SerGluHisValValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSer	706
Db	2183	TTGCAAGAGGGCGTGGAGGTTCCTCTCCGCACTCGCAGCGGCTCTCCAGAAATCAAC	2242

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 16, 2005, 23:13:19 ; Search time 419 Seconds
(without alignments)

4256.663 Million cell updates/sec

Title: US-09-833-222A-10

Perfect score: 5726

Sequence: 1 MAVALGTRRRDRYKLVADTF.....MPMNTVPVVLGGNIRVYAL 1090

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=Bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-USER=US09833222@cgn 1.1 89 @runat_15112005_145359_15799 -NCPUS=6 -ICPU=3
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Database :

Issued Patents NA.*
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3416.5	59.7	3276	4	US-10-162-012-16
2	3416.5	59.7	3690	4	US-10-162-012-14
3	3410.5	59.6	3770	4	US-09-397-550-21
4	3400.5	59.4	3213	4	US-09-397-550-9
5	3326.5	58.1	3114	4	US-09-397-550-8
6	3278.5	57.3	3057	4	US-09-397-550-7
7	1792.5	31.3	1050	4	US-09-397-550-15
8	1695	29.6	969	4	US-09-397-550-14
9	1598	27.9	912	4	US-09-397-550-13
10	1188.5	20.8	5279	3	US-09-470-443-5
11	1187.5	20.7	5463	3	US-09-470-443-1
12	1187.5	20.7	5482	3	US-09-470-443-3

13	1187.5	20.7	5482	4	US-09-397-550-19
14	1179.5	20.6	3327	4	US-09-397-550-3
15	1158.5	20.2	3248	4	US-09-397-550-2
16	1150.5	20.1	3186	4	US-09-397-550-1
17	1089	19.0	3802	1	US-08-404-354B-2
18	1089	19.0	3802	1	US-08-314-083B-2
19	1089	19.0	3802	1	US-08-435-675B-2
20	1089	19.0	3802	3	US-08-884-599-2
21	1088	19.0	3802	1	US-08-336-257A-4
22	1084	18.9	3579	1	US-08-455-543A-36
23	1084	18.9	3579	2	US-08-193-078B-25
24	1084	18.9	3579	2	US-08-223-305C-36
25	1084	18.9	3579	3	US-08-949-386-32
26	1084	18.9	3579	3	US-08-450-562-32
27	1084	18.9	3579	3	US-08-984-709A-32
28	1084	18.9	3579	3	US-08-450-273-32
29	1084	18.9	3579	4	US-08-450-273-32
30	1079.5	18.9	3636	1	US-08-455-543A-32
31	1079.5	18.9	3636	2	US-08-193-078B-22
32	1079.5	18.9	3636	2	US-08-223-305C-32
33	1079.5	18.9	3636	3	US-08-949-386-29
34	1079.5	18.9	3636	3	US-08-450-562-29
35	1079.5	18.9	3636	3	US-08-984-709A-29
36	1079.5	18.9	3636	3	US-08-450-272-29
37	1079.5	18.9	3636	4	US-08-450-273-29
38	1077.5	18.8	3566	1	US-07-745-206A-24
39	1077.5	18.8	3566	2	US-08-311-363-24
40	1077.5	18.8	3600	1	US-08-455-543A-11
41	1077.5	18.8	3600	1	US-08-455-543A-33
42	1077.5	18.8	3600	2	US-08-193-078B-11
43	1077.5	18.8	3600	2	US-08-223-305C-11
44	1077.5	18.8	3600	2	US-08-223-305C-33
45	1077.5	18.8	3600	2	US-08-149-097D-11

ALIGNMENTS

RESULT 1

US-10-162-012-16
; Sequence 16, Application US/10162012
; Patent No. 6682597
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
; FILE REFERENCE: 10448-190001
; CURRENT APPLICATION NUMBER: US/10/162,012
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/209,845
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: US 09/875,321
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: PCT/US01/18340
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,423
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18398
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,238
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,363
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18247
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/227,068
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 09/928,530
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/25475
; PRIOR FILING DATE: 2001-08-15

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; PRIOR APPLICATION NUMBER: US 60/226,770
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/934,421
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/US01/26096
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/279,281
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 10/109,029
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: PCT/US02/09728
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/290,288
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US (not assigned)
; PRIOR FILING DATE: 2002-05-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 3276
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-162-012-16

Alignment Scores:
Pred. No.: 0 Length: 3276
Score: 3416.50 Matches: 628
Percent Similarity: 77.81% Conservative: 189
Best Local Similarity: 59.81% Mismatches: 212
Query Match: 59.67% Indels: 22
DB: 4 Gaps: 7

US-09-833-222A-10 (1-1090) x US-10-162-012-16 (1-3276)
QY 13 ValLysLeuTrpAlaAspThrPheGlyAspLeuTyrAsnThrValThrLysTyrSer 32
DB 124 GTAAAGCTCTGGGCGCTGCTTTTGGTGGGAGATAAAATCCATTCGTGCTAAAGTACTCC 183
QY 33 GlySerLeuLeuGluGlnLysLysTyrLysAspValGluSerSerLeuLysIleGluGlu 52
DB 184 GGTTCACAGCTTCTGCNAAAGAAATACAAAGATATGAGAAAGACGTTGGCCATAGAGAA 243
QY 53 ValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArgArg 72
DB 244 ATTGATGGCTTCAACTGGTAAAGAGCTCGCCAAAGAACATGAGAGATGTTTCACAAG 303
QY 73 LysValGluAlaValGlnAsnLeuValGluAlaGluAlaGluAlaAspLeuAsnHisGlu 92
DB 304 AAGTCTGAGGCCCTCAGGCGCTCTGGTGGAGGCTGCAGAGAGACACACCTGAAACATGAA 363
QY 93 PheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArgAspGlu 112
DB 364 TTTGATGCAGACTTACAGTATGAAATCTTCATGCTGCTGATAAATGAAAGGACAAA 423
QY 113 LysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHisPheSer 132
DB 424 GACGGGAAATTTTGGAGCTGGGAAAGGAATTCATCTAGCCCCCAAAATGACCAATTTTAA 483
QY 133 AsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyrAsnLys 152
DB 484 AATTTGCTGTGAACATCAGCTTAAGTGACGTCCTCAAGTACCAACGACATGTACAAACAAA 543
QY 153 AspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPheValGlu 172
DB 544 GACCTTGCATTTGCTAATGGGTTTATTTGGTCTGAATCTCTAAACAAAGTTTGTAGAT 603
QY 173 AsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhePhe 192
DB 604 AACTTTGACCGTGACCCATCTCTCATATGCGAGTACTTTTGGAAAGTGCAAAGGCGCTTTT 663
QY 193 ArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPheAspCys 212
DB 664 AGCAGTATCCCGGGATTAATATGGGAAACCATGATGAGAAATGGAGTCAATTCCTTCGACTGC 723
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QY 213 AtqAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIleLeuVal 232
DB 724 AGGAACCGAAATGGTACATCCAGGAGCAAACTTCCGAAAGACGGTGGTCAATTTAGTT 783
QY 233 AspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThrThr 252
DB 784 GACGTCAAGTGGCAGCATGAAGGACTCCGCTGCTGACTATCGGAAGCAACAGTCTCATCC 843
QY 253 IleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAspTyrVal 272
DB 844 ATTTTGGATACACTTGGGATGATGACTTCTTCAACATAATTCCTTATAATGAGGAGCTT 903
QY 273 HisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsnArgGlu 292
DB 904 CACTATGTGAACCTTTCCTGTAATGGAACCTTTGGTCAAGCCACAGGACAAACAAAGAG 963
QY 293 HisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAspGlnAla 312
DB 964 CACTTCAGGGAGCATCTGGACAAACCTTTTCGCCCAAGGAATTCGAATGTTGGATATAGCT 1023
QY 313 LeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySerLeuCys 332
DB 1024 CTGAATGAGGCCCTTCAACATTCCTGAGTGATTTCAACACACACGCGGACCAAGCAATATCTGC 1083
QY 333 AsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProValPheGlu 352
DB 1084 AGTCAGGCCCATCATGCTCATTAATCTGATGGGGGGTGGACACCTATGATACATACTTTTGGCA 1143
QY 353 LysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArgGluVal 372
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QY 373 SerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThrGlnIle 392
DB 1204 GCGTTTGCAGACAATCTAAAGTGGATGGCTCTGCCAACAAAGGATTTTATACCCAGATC 1263
QY 393 SerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSerArgPro 412
DB 1264 TCACCTTGCTGTGATGTCAGGAGATGTCATGGAATACCTTCACGTGCTTAGCCGGCCC 1323
QY 413 MetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSerLysLeu 432
DB 1324 AAAAGTCATCGACGAGGATGATGTGGTGTGGACCGAAGCTTACATTTGACAGCACTCTC 1383
QY 433 LeuSerSerGlnAlaGlnSerLeuThr-----LeuLeuThrThrVal 446
DB 1384 -----CCTCAGGCACAAAGCTGATGATGATCAGGCGCCGCTCCTGATGACCACTGTA 1437
QY 447 AlaMetProValPheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyVal 466
DB 1438 GCCATGCCCTGTGTTAGTAAAGCAGAACCAACAGATCGAAGGCATTTCTCTGGGAGTG 1497
QY 467 ValGlySerAspValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGly 486
DB 1498 GTTGGCACAGATGTCCAGTGAAGAACTTCTGGAAGACCATCCCAAAATACAAGTTAGGG 1557
QY 487 ValHisGlyTyrAlaPheLeuAsnThrAsnAsnGlyTyrIleIleuSerHisProAspLeu 506
DB 1558 ATTTCAGGTTATGCTTTGCAATCAAAATAATGATATATCTGACGATCCGGAACCTC 1617
QY 507 ArgProLeuTyrArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAsp 526
DB 1618 AGGCTGCTGTACGAAGAGNAAAAAG---CGAAGGAACCTTAACATATAGTAGCGTTGAC 1674
QY 527 LeuSerGluValGluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArg 546
DB 1675 CTCTCTGAGGTGGAGTGGGAGACCGGATGACGCTGTGAGAAATGCTATGTTGGTAATCGA 1734
QY 547 GluThrGlyThrLeuSerMetAspValLysValProMetAspLysGlyValArgValLeu 566
DB 1735 AAAGCGGGGAAGTTTTCATGGAGGTGAAGAAAGACAGTGGACAAAGGGGAAACGGGTTTG 1794
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[illegible]

Db	2866	ACAGCTAAAGCC-----CAGAAATTGAAACAGACCCCTGGAGCCT	2904
Qy	947	CysAspThrGluTyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIle	965
Db	2905	TGTGATACTCAATATCCAGCATTCGTCTCTGAGCGCCACCATCAAGGAGACTACAGGGAAT	2964
Qy	967	ValGluCysGlyProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLeu	986
Db	2965	ATTGCTTGTGAAGACTGCTCTCAAGTCTTTGTTCATCCAGAGAAATCCCAAGCAGCAACCTG	3024
Qy	987	LeuLeuLeuValThrAspProThrCysAspCysSerIlePheProProValLeuGlnGlu	1006
Db	3025	TTCATGTGTGTGGACAGAGCTGCCTCTGTGAATCTCTGGCCCCCATCACCATGGCA	3084
Qy	1007	AlaThrGluValLysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeu	1026
Db	3085	CCCATTGAATCAGGTATATGAATCCCTTAAGTGTGAACGTCTAAAGGCCGAGAAGATC	3144
Qy	1027	ArgArgArgProAspSerCysHisAlaPheHisProGluValArgValGluAlaAspArg	1046
Db	3145	AGAAGGCCCGCAGAATCTTGTTCATCTGGCTTCATCTCTGAG-----GAGAATGCAAGGGAG	3198
Qy	1047	GlyTTrpAlaGlyPheSerSerProAsnPro	1056
Db	3199	TG-TGGGGGTGCGCCGAGTCTCCAAGCCCA	3227
RESULT 2			
US-10-162-012-14			
; Sequence 14, Application US/10162012			
; Patent No. 6682597			
; GENERAL INFORMATION:			
; APPLICANT: Curtis, Rory A.J.			
; APPLICANT: Silos-Santiago, Immaculada			
; APPLICANT: Gu, Wei			
; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS			
; FILE REFERENCE: 10448-190001			
; CURRENT APPLICATION NUMBER: US/10/162,012			
; CURRENT FILING DATE: 2002-06-04			
; PRIOR APPLICATION NUMBER: US 60/209,845			
; PRIOR FILING DATE: 2000-06-06			
; PRIOR APPLICATION NUMBER: US 09/875,321			
; PRIOR FILING DATE: 2001-06-06			
; PRIOR APPLICATION NUMBER: PCT/US01/18340			
; PRIOR FILING DATE: 2001-06-06			
; PRIOR APPLICATION NUMBER: US 60/209,257			
; PRIOR FILING DATE: 2000-06-05			
; PRIOR APPLICATION NUMBER: US 09/875,423			
; PRIOR FILING DATE: 2001-06-05			
; PRIOR APPLICATION NUMBER: PCT/US01/18398			
; PRIOR FILING DATE: 2001-06-05			
; PRIOR APPLICATION NUMBER: US 60/209,238			
; PRIOR FILING DATE: 2000-06-05			
; PRIOR APPLICATION NUMBER: US 09/875,363			
; PRIOR FILING DATE: 2001-06-05			
; PRIOR APPLICATION NUMBER: PCT/US01/18247			
; PRIOR FILING DATE: 2001-06-05			
; PRIOR APPLICATION NUMBER: US 60/227,068			
; PRIOR FILING DATE: 2000-08-22			
; PRIOR APPLICATION NUMBER: US 09/928,530			
; PRIOR FILING DATE: 2001-08-13			
; PRIOR APPLICATION NUMBER: PCT/US01/25475			
; PRIOR FILING DATE: 2001-08-15			
; PRIOR APPLICATION NUMBER: US 60/226,770			
; PRIOR FILING DATE: 2000-08-21			
; PRIOR APPLICATION NUMBER: US 09/934,421			
; PRIOR FILING DATE: 2001-08-21			
; PRIOR APPLICATION NUMBER: PCT/US01/26096			
; PRIOR FILING DATE: 2001-08-21			
; PRIOR APPLICATION NUMBER: US 60/279,281			
; PRIOR FILING DATE: 2001-03-28			
; PRIOR APPLICATION NUMBER: US 10/109,029			
; PRIOR FILING DATE: 2002-03-28			


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; PRIOR APPLICATION NUMBER: PCT/US02/09728
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/290,288
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US (not assigned)
; PRIOR FILING DATE: 2002-05-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 3690
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29)...(3301)
US-10-162-012-14

Alignment Scores:
Pred. No.: 0 Length: 3690
Score: 3416.50 Matches: 628
Percent Similarity: 77.81% Conservative: 189
Best Local Similarity: 59.81% Mismatches: 212
Query Match: 59.67% Indels: 22
DB: 4 Gaps: 7

US-09-833-222A-10 (1-1090) x US-10-162-012-14 (1-3690)

QY 13 ValLysLeuTrpAlaAspThrPheGlyAspLeuTyrAsnThrValThrLysTyrSer 32
DB 152 GTGAAGCTCTGGGCGCTTGGTGGGGAGATAAAATCCATTCGTGTAAAGTACTCC 211
QY 33 GlySerLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysLysLeuGlu 52
DB 212 GGTTCACAGCTTCTGCAAGAAGAAATACAAAGATGATGAGAAAGACGTTGTCATAGAAGAA 271
QY 53 ValAspGlyLeuGluLeuValAlaArgLysPheSerGluAspMetGluAsnMetLeuArgArg 72
DB 272 ATTGATGGCTCCAACTGGTAAAGAGCTGGCAAGAACATGCAAGAGAGATGTTTCACAAG 331
QY 73 LysValGluAlaValGlnAsnLeuValGluAlaAlaGluAlaAspLeuAsnHisGlu 92
DB 332 AAGTCTGAGCGCTGACGGCTCTGGTGGAGGCTGCAGAAAGAACACACCTGAAACATGAA 391
QY 93 PheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuLeuLeuAsnGluArgAspGlu 112
DB 392 TTTGATGCACACTTACAGTATGAACTTCAATGCTGTGCTGATTAATGAAGGGACAAA 451
QY 113 LysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHisPheSer 132
DB 452 GACGGGAATTTTGGAGCTGGGAAAGGAATTCATCTTAGCCCCCAAATGACCACTTTTAAT 511
QY 133 AsnLeuProValAsnThrSerLysSerValGlnLeuProThrAsnValTyrAsnLys 152
DB 512 AATTGGCTGTGAACATCAGCTTAAGTGACGTCCAAGTCAACAGCAACATGTGTAACAAA 571
QY 153 AspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPheValGlu 172
DB 572 GACCTGCAATTTGCAATGGGTTTATGTGCTGTAATCTCTAAACAAAGTTTGTAGAT 631
QY 173 AsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhePhe 192
DB 632 AACTTTGACCGTACCCTCTCTCATATGGCAGTACTTTTGAAGTGCMAAGGGGCTTTT 691
QY 193 ArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPheAspCys 212
DB 692 AGCAGTATCCGGGGATTAAATGGGAACCAAGATGAGAAATGGATGCTATTCCTTCGACTGC 751
QY 213 ArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIleLeuVal 232
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QY 233 AspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThrThr 252
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Qy 607 LeuHisAspLeuLeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThr 626
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Qy 647 ArgLysAspProAspLeuGluCysAspGluLeuValArgGluValLeuPheAspAla 666
Db 2063 GGCAAGAACCTCTGCTCCAGTGTGATTAAGAATGATCCAGAGCTCTCTTTGACGGC 2122
Qy 667 ValValThrAlaProMetGluAlaTyrTrpThrAlaLeuAlaLeuAlaMetSerGluGlu 686
Db 2123 GTGGTAGTGCCTCCATTAAGCGTATTGGACCAAGCTGGCCCTCAACAAATCTGAAAT 2182
Qy 687 SerGluHisValValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSer 706
Db 2183 TCTGACAAAGGCGTGGAGGTTGCTCTCGGCACCTCGCAGGCGCTCTCAGAAATCAAC 2242
Qy 707 LeuPheValGlySerGluLysValSerAspArgLysPheLeuThrProGluAspGluAla 726
Db 2243 CTGTTGTGGGGCTGAGCAGCTCACCAATCAGACCTTCCTGAAAGCTGGCGCAAGGAG 2302
Qy 727 SerValPheThrLeuAspArgPheProLeuTrpTyrArgGlnAlaSerGluHisProAla 746
Db 2303 AACATTTTAAACGCAGACCATTTCCCTCTCTGTTACCGAAGAGCGCTGAGCAGATTCCA 2362
Qy 747 GlySerPheValPheAsnLeuArgTrpAlaGluCysProGluSerAlaGlyGluProMet 766
Db 2363 GGGAGCTTCGTCTACTCGATCCCAATCAGCAGCTGGACCA-----GTCAATAAAGCAAT 2416
Qy 767 ValValThrAlaSerThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAla 786
Db 2417 GTGGTGACAGCAAGTACATCATCAGCTCTCGATGAACGAAATCTCTGTGGTGCGCA 2476
Qy 787 AlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArg 806
Db 2477 GCTGTAGGCATTACAGTGAATTTGAATTTTCCAAAGGAAGTTCTCGACTGCGCAGCAGA 2536
Qy 807 GlnCysSerThrValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCys 826
Db 2537 CAGTGTGCTTCCCTGGATGGCAATGCTCCATCAGCTGTGATGATGAGACTGTGAATTTGT 2596
Qy 827 PheValIleAspAsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArg 846
Db 2597 TACCTCATAGCAATATAGATTTATTTTGGTGTCTGAAGACTACACAGACTGGAGAC 2656
Qy 847 PheLeuGlyGluValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSer 866
Db 2657 TTTTGTGGTGGAGAGCTGTGATGAACAAATTTGCTAACAAATGGGCTCTTTTAA 2716
Qy 867 GlnValThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisSerAla 886
Db 2717 AGAATTAACCTTTATGATACCAAGCAGCATGTGTAGAGCCCAACAAAGAAAGCAGCATGGC 2776
Qy 887 AlaGlnProLeuValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuGln 906
Db 2777 GCCCATGGCTCTCGGATCCCTTATATGCTCTCTCTGATGATGATGATGATGATGATGATG 2836
Qy 907 GluLeuValLeuPheLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAla 926
Db 2837 GAATCTGCTTGTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2893
Qy 927 GluAlaLysSerValPheHisHisSerHisLysLysLysGlnAspProLeuGlnPro 946
Db 2894 ACAGCTAAAGCC-----CAGAAATTGAACAGACCCCTGGAGCCT 2932
Qy 947 CysAspThrGluTyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIle 966
Db 2933 TGTGATACTGATATCCAGCATTCCTCTGAGGCGCACCATCAAGGAGACTACAGGGAAT 2992

Qy 967 ValGluCysGlyProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLeu 986
Db 2993 ATTGCTTGTGAAGACTGCTCCAAAGTCTTTTGTCTCCAGCAAAATCCCAAGCAGCAACCTG 3052
Qy 987 LeuLeuLeuValThrAspProThrCysAspCysSerIlePheProProValLeuGlnGlu 1006
Db 3053 TTCATGTGTGTGGTGGACAGCAGCTGCTCTGTAATCTGTGGCCCCCATCACCATGGCA 3112
Qy 1007 AlaThrGluValLysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeu 1036
Db 3113 CCCATTGAATCAGGTATATGAATCCCTTAAGTGTGAACGTCTTAAAGGCCCAAGATC 3172
Qy 1027 ArgArgArgProAspSerCysHisAlaPheHisProGluValArgValGluAlaAspArg 1046
Db 3173 AGAAGGCCCCAGATCTTGTCTGCTTCCATCTCTGAG-----GAGAATGCAAGGGAG 3226
Qy 1047 GlyTrpAlaGlyPheSerSerProAsnPro 1056
Db 3227 TG-TGGGGTGGCCGAGTCTCCAAGCCCA 3255
RESULT 3
US-09-397-550-21
; Sequence 21, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCE: 180
; CURRENT APPLICATION NUMBER: US/09/397,550
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-397-550-21
Alignment Scores:
Pred. No.: 0 Length: 3770
Score: 3410.50 Matches: 624
Percent Similarity: 77.87% Conservative: 189
Best Local Similarity: 59.77% Mismatches: 216
Query Match: 59.56% Indels: 16
DB: 4 Gaps: 6
US-09-833-222A-10 (1-1090) x US-09-397-550-21 (1-3770)
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Qy 33 GlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIleGluGlu 52
Db 327 GGTTCACGCTCTTGCAGAAAGAAATACAAAGAGATATGAGAAAGACGTTGCCATAGAAGAA 386
Qy 53 ValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArgArg 72
Db 387 ATTGATGGCTCTCACTGGTAAAGAGCTGGCAAGAACATGAGAGATGTTTTCACAG 446
Qy 73 LysValGluAlaValGlnAsnLeuValGluAlaGluGluAlaAspLeuAsnHisGlu 92
Db 447 AAGTCTGAGGCGCTCAGGCGTCTGGTGGAGCTGCAGAGGAGCAGACACCTGAAACATGAA 506
Qy 93 PheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArgAspGlu 112
Db 507 TTTGATGCGACTTACAGTATGAATACTTCAATGCTGTGCTGATAAATGAAGAGGACAA 566
Qy 113 LysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHisPheSer 132
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[illegible]

RESIT.T 4

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US-09-397-550-9
; Sequence 9, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCE: 180
; CURRENT APPLICATION NUMBER: US/09/397,550
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 3213
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-397-550-9

Alignment Scores:
Pred. No.: 0 Length: 3213
Score: 3400.50 Matches: 620
Percent Similarity: 78.12% Conservative: 187
Best Local Similarity: 60.02% Mismatches: 207
Query Match: 59.39% Indels: 19
DB: 4 Gaps: 6

US-09-833-222A-10 (1-1090) x US-09-397-550-9 (1-3213)

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Db      1204  GCGTTTCAGACAATCTAAGATGGATGGCTGTGCCAACAAGGATTTTACCAGATC 1263
Qy      393  SerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSerArgPro 412
Db      1264  TCCACCTTGGCTGATGTGTCAGGAGAAATGTATCATGAAATACCTTCACGTGTAGCGGCC 1323
Qy      413  MetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSerLysLeu 432
Db      1324  AAGTCTATCACCAGGAGCATGATGTGTGGACCGAAGCTTACATTGACAGACTCTG 1383
Qy      433  LeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProValPheSer 452
Db      1384  ACTGATGATCAGGCGCCCC-----GTCCCTGATGACCACCTGTAGCCATGCTGTGTAGT 1437
Qy      453  LysValSerGlnThrArgSerHisGlyIleLeuLeuGlyValValGlySerAspValAla 472
Db      1438  AAGCAGAACCAACCCAGATCGAAGGGCATTTCTTCTGGGAGTGGTTGGCACAGATGCCCA 1497
Qy      473  LeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyrAlaPhe 492
Db      1498  GTGNAAGAACTTCTGAAGACCATCCCAATACAACTTAGGGATTACGGTTATGCGCTTT 1557
Qy      493  LeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyrArgGlu 512
Db      1558  GCAATCACAATAATAGRTATATCTGACGCATCCGGAACTCAGGCTGCTGTACGAAGAA 1617
Qy      513  GlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluValGluTrp 532
Db      1618  GGAATAAAG---CGAAGAAACCTTAACATATAGTACGCTTGACCTCTCTGAGGTGGAGTG 1674
Qy      533  GluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThrLeuSer 552
Db      1675  GAAGACCGAGATGACGTGTGTGAGAAATGCTATGTGTGAATCGAAGACCGGGAAGTTTCC 1734
Qy      553  MetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsnAspTyr 572
Db      1735  ATGGAGGTGAAGAAGACAGTGGACAAAGGCAAAACGGGTTTTGGTGATGACAAATGACTAC 1794
Qy      573  PhePheThrAspLysSerAspThrProPheSerLeuGlyAlaValLeuSerArgGlyHis 592
Db      1795  TATTATACAGACATCAAGGTACTCTCTTTCAGTTTTAGGTGTGGCGCTTTCCACAGGTGAT 1854
Qy      593  GlyGluTyrIleLeuLeuGlyValAsnThrSerValGluGluGlyLeuHisAspLeuHis 612
Db      1855  GGGAAATATTTCTCCGAGGGAATGTAAACCATCGAAGAGGCTGCACTGACTTAGAACAT 1914
Qy      613  ProAspLeuAlaLeuAlaGlyAspTyrIleTyrCysIleThrAspIleAspProAspHis 632
Db      1915  CCGAGTGTGCTTGGCAGATGAATGGTCTCTACTGCAACACTGACCTACACCCCTGAGCAC 1974
Qy      633  ArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspProAspLeu 652
Db      1975  CGGCATCTGTCTCAGTTAGAGCGGATTAAGCTCTACCTAAAGGCCAAAGAACCTCTGCTC 2034
Qy      653  GluCysAspGluGluLeuValArgGluValLeuPheAspAlaValValThrAlaProMet 672
Db      2035  CAGTGTGATAAGAAATGTATCCAGAAAGTCTCTTTTGACCGGTGTGTAGTGTGCCCCATT 2094
Qy      673  GluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisValValAsp 692
Db      2095  GAAGCGTATTGGACCGACTGGCCCTCAACAAATCTGAAAAATCTGACAAAGGGCGTGGAG 2154
Qy      693  MetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGlySerGlu 712
Db      2155  GTTGCCCTTCTCGGCATCTCGACCGGGCTCTCCAGAAATCAACCTGTGTGTGGGGGTGAG 2214
Qy      713  LysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThrLeuAsp 732
Db      2215  CAGCTCACCAATCAGGACTTCTCGAAAGCTGGCGACAAGGAGAACATTTTAAACGCAGAC 2274
Qy      733  ArgPheProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheValPheAsn 752
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Db      2275  CATTTCCCTCTCTGGTACCAGAGCGCTGAGCAGATTCACGGGAGCTTCGTCTACTCG 2334
Qy      753  LeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAlaSerThr 772
Db      2335  ATCCCAATTCAGCACTCGACCA-----GTCAATAAAGCAATGTGTGGTACAGCAAGTACA 2388
Qy      773  AlaValAlaValThrValAspLysArgThrAlaIleAlaAlaAlaAlaGlyValGlnMet 792
Db      2389  TCCATCCAGCTCTCTGGATGNAACGGAATCTCTGTGGTGGCAGCTGTAGGCATTTCAGATG 2448
Qy      793  LysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThrValAsp 812
Db      2449  AAACCTTGAATTTTCCAAAGGAAGTTCTGGACTCGCCAGCAGACAGTGTGCTCCCTGGAT 2508
Qy      813  GlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAspAsnAsn 832
Db      2509  GGCAATGCTCCATCAGCTGTGATGATGAGACTGTGAATTTGTACCTCATAGACAATAAT 2568
Qy      833  GlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGluValAsp 852
Db      2569  GGATTTATTTTGGTGTCTGAAGACTACACAGACTGGAGACTTTTGTGTGAGATCGAG 2628
Qy      853  GlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMetTyrAsp 872
Db      2629  CGAGCTGTGATGAACAAATTTGCTTAAACAATGGGCTCCTTTAAAAAGAATTTACCTTTATGAC 2688
Qy      873  TyrGlnAlaMetCysLysProSerSerHisHisSerAlaAlaGlnProLeuValSer 892
Db      2689  TACCAAGCCATGTGTAGAGCCAAACAGGAAAGCAGCGATGGCGCCCATGGCCCTCTCGAT 2748
Qy      893  ProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValLeuPheLeu 912
Db      2749  CCTTATAATGCTCTCTCTCTGAGTAAATGGATCATGACAGAACTTGTCTTGTTCCTG 2808
Qy      913  LeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSerValPhe 932
Db      2809  GTGGAATTTAAACCTCTGCG---AGTTGTGGCACTCCGATATGACAGCTAAAGCC----- 2859
Qy      933  HisHisSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGluTyrPro 952
Db      2860  -----CAGAAATTTGAACACAGACCCCTGGAGCCTTGTGATCTGTAATATCCA 2904
Qy      953  ValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGlyProCys 972
Db      2905  GCATTCTGCTCTGAGCGCACCATCAAGGAGACTACAGGGAATATTGCTGTGGAAGACTGC 2964
Qy      973  GlnLysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuValThrAsp 992
Db      2965  TCCAAGTCTCTTTGTCTATCCAGCAAAATCCCAAGCAGCAACCTGTTCATGTGGTGGTGAC 3024
Qy      993  ProThrCysAspCysSerIlePheProProValLeuGlnGluAlaThrGluValLysTyr 1012
Db      3025  AGCAGCTGCTCTGTGAATCTGTGGCCCCCATCACCATGGCACCCCATTTGAAATCAGGTAT 3084
Qy      1013  AsnAlaSerValLysCysAspArgMet-----ArgSerGlnLysLeu 1026
Db      3085  AATGAATCCCTTAAGTGTGAACGCTCTAAAGGCCCCAGAGAATCAGAAGGCCCAAGAAGATC 3144
Qy      1027  ArgArgArgProAspSerCysHisAlaPheHisProGlu 1039
Db      3145  AGAAGCGGCCCAAGAATCTTGTGTCATGGCTTCCATCTCTGAG 3183

RESULT 5
US-09-397-550-8
; Sequence 8, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCE: 180
; CURRENT APPLICATION NUMBER: US/09/397,550
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; CURRENT FILING DATE: 1999-09-16
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 8
 ; LENGTH: 3114
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-397-550-8

Alignment Scores:

Pred. No.: 0 Length: 3114
 Score: 3326.50 Matches: 606
 Percent Similarity: 78.32% Conservative: 185
 Best Local Similarity: 60.00% Mismatches: 206
 Query Match: 58.09% Indels: 13
 DB: 4 Gaps: 5

US-09-833-222a-10 (1-1090) x US-09-397-550-8 (1-3114)

Qy 13 ValLysLeuTrpAlaAspThrPheGlyAspLeuTyrAsnThrValThrLysTyrSer 32
 Db 124 GTGAAGCTCTGGGCTCGGCTTTGGTGGGAGATAAAATCCATTGCTGCTAAGTACTCC 183
 Qy 33 GlySerLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysLysGlu 52
 Db 184 GGTTCAGCTTCTGCAAAAGAAATACAAAGATGATGAGAAAGACGTTGCCATAGAGAA 243
 Qy 53 ValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArg 72
 Db 244 ATTGATGGCTTCCAACTGGTAAAGAGCTGCGAAGAACATGGAAGAGATGTTTCAAG 303
 Qy 73 LysValGluAlaValGlnAsnLeuValGluAlaGluAlaAspLeuAsnHisGlu 92
 Db 304 AAGTCTGAGCGCTGAGCGCTGCTGGTGGAGCTGCAGAGAGACACACCTGAAACATGAA 363
 Qy 93 PheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuLeuLeuAsnGluArgAspGlu 112
 Db 364 TTTGATCGACACTTACAGTATGATCTTCAATGCTGTGCTGATAAATGAAGGGACAAA 423
 Qy 113 LysGlyAsnPheValGluLeuGlyValGluPheLeuLeuGluSerAsnAlaHisPheSer 132
 Db 424 GACGGGAATTTTTGGAGCTGGGAAGGAATTCATCTAGCCCCAAATGACCATTTTAA 483
 Qy 133 AsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyrAsnLys 152
 Db 484 AATTGCTGTGAACATCAGTCTAAGTGACGCTCAAGTACCACGAACAGATGTACAAACA 543
 Qy 153 AspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPheValGlu 172
 Db 544 GACCTGCAATTTGTCAATGGGGTTTATTTGGTCTGAAATCTCTAAACAAAGTTTTGTAGAT 603
 Qy 173 AsnPheGlnArgAspProThrLeuThrTyrGlnTyrPheGlySerAlaThrGlyPhePhe 192
 Db 604 AACTTTGACCGTGACCATCTCTCATATGGCAGTACTTTTGAAGTGCAGAGGGCTTTTT 663
 Qy 193 ArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPheAspCys 212
 Db 664 AGCAGTATCCGGGATTAATGGGAACCATGAGATGAGATGAGTCAATTCGCTTCGACTGC 723
 Qy 213 ArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIleLeuVal 232
 Db 724 AGGAACCGAAATGGTATACATCCAGGACCAACTTCTCCGAAAGACGTTGCTTATAGTT 783
 Qy 233 AspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThrThr 252
 Db 784 GACCTAGTGACATGAAAGGACTCCGCTGACTATCCGAAAGACAAACAGTCTCACTCC 843
 Qy 253 IleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAspTyrVal 272
 Db 844 ATTTTGGATACACTTGGGATGATGACTTCTTCAACATAATTCGCTTATATAGGAGCTT 903
 Qy 273 HisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsnArgGlu 292

Db 904 CACTATGTGGAACCTTGCCCTGGAATGAACTTTGGTCAAGCCACAGGACAAACAAAGAG 963
 Qy 293 HisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAspGlnAla 312
 Db 964 CACTTCAGGAGCATCTGGACAAACTTTTCGCAAAAGGAATTTGGAATGTTGGATATAGT 1023
 Qy 313 LeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySerLeuCys 332
 Db 1024 CTGAATGAGGCTTCAACATTTCTGAGTGATTTTCAACCCACACGGGACAAAGAGTATCTGC 1083
 Qy 333 AsnGlnAlaIleMetLeuIleSerAspGlyValValAspTyrGluProValPheGlu 352
 Db 1084 AGTCAGCCCATCATGCTCATGATGGGCGGTGACACCTATGATACAAATTTTGCA 1143
 Qy 353 LysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArgGluVal 372
 Db 1144 AATACAAATTTGGCCAGATCGAAAGTTTCGATCTTCACATACCTCATTTGGACGAGGCT 1203
 Qy 373 SerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrThrGlnIle 392
 Db 1204 GCGTTTGCAGACAATCTAAAGTGGATGGCTGTGCCAACAAAGGATTTTATCCCGACATC 1263
 Qy 393 SerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSerArgPro 412
 Db 1264 TCCACTTGGCTGATGTCAGGAGAAATGTCATGGAATACCTTCACGTGCTTAGCGGCC 1323
 Qy 413 MetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSerLysLeu 432
 Db 1324 AAGTCATCGACAGGAGCATGATGGTGTGGACCGAAGCTTACATTTGACAGCACTCTG 1383
 Qy 433 LeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrValAlaMetProValPheSer 452
 Db 1384 ACTGATGATCAGGCGCCCC-----GTCCTGATGACCACTGTAGCCATGCTGTGTAGT 1437
 Qy 453 LysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAspValAla 472
 Db 1438 AAGCAAGCAACCAACAGATCGAAGGCAATCTCTTGGAGTGGTTGGCAGATGTCCCA 1497
 Qy 473 LeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyrAlaPhe 492
 Db 1498 GTGAAGAACTTCTGAAGACCATCCCAAAATACAAAGTTAGGGATTACGGTTATGCTTT 1557
 Qy 493 LeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyrArgGlu 512
 Db 1558 GCAATCACAAATTAATGRTATATCTCGACGATCCGGAACCTAGGCTGTGTACGAAGAA 1617
 Qy 513 GlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluValGluTyr 532
 Db 1618 GGAAGAAAG---CGAAGGAACCTTAATAGTAGGCTTGACCTCTCTGAGTGGAGTGG 1674
 Qy 533 GluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThrLeuSer 552
 Db 1675 GAAGACCGAGATGACGCTGTTGAAATGCTATGTAATCGAAGACGGGGAAGTTTTC 1734
 Qy 553 MetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsnAspTyr 572
 Db 1735 ATGGAGGTGAAGAGACAGTGGACAAAGGGAACCGGTTTGTGTATGACAAATGACTAC 1794
 Qy 573 PhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArgGlyHis 592
 Db 1795 TATTATACAGATCAAGGGTACTCTCTTTCAGTTTAGTGGGCTTTTCAGAGGTTCAT 1854
 Qy 593 GlyGluTyrIleLeuLeuGlyAsnThrSerValGluGlyLeuHisAspLeuLeuHis 612
 Db 1855 GGAATATATTTCTCCGAGGGAATGTAACCATCGAAGAGGCTGCTGATGACTTAGAACAT 1914
 Qy 613 ProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspProAspHis 632
 Db 1915 CCCGATGTGCTTGGCAGATGAATGGTCTCTACTGCAACACTGACCTACACCTTGAGCAC 1974
 Qy 633 ArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspProAspLeu 652
 Db 1975 CGCCATCTGTCTCAGTTAGAACGATTAAGCTCTTACCTAAAGCAAGAACCTCTGCTC 2034

Qy	653	GluCysAspGluGluLeuValArgGluValLeuPheAspAlaValThrAlaProMet	672
Db	2035	CAGTGTGATAAAGAATTGATCCAAGAAGTCCTTTTTCAGCGGTGTGAGTGCGCCCAT	2094
Qy	673	GluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisValValAsp	692
Db	2095	GAAGCGTATTGGACAGCGCTGGCCCTCAACAAATCTGAAATCTGCAAGGGCGGTGGAG	2154
Qy	693	MetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGlySerGlu	712
Db	2155	GTTGCCCTCTCGGCATCTCGACCGGCCTCTCCAGAATCAACCTGTTGTTCGGGGCTGAG	2214
Qy	713	LysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThrLeuAsp	732
Db	2215	CAGCTCACCAATCAGGACTTCTGAAAGCTGGCAGCAAGGAGAACATTTTAAACGCAGAC	2274
Qy	733	ArgPheProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheValPheAsn	752
Db	2275	CATTTCCTCTCTCGTACCGAAGACCGCTGAGCAGATTCACAGGAGCTTCGTCTACTCG	2334
Qy	753	LeuArgTrpAlaGluGlyProGluSerAlaGlyLeuProMetValValThrAlaSerThr	772
Db	2335	ATCCCATTCAGACTGGACCA-----GTCATTAAGAAGCAATGTGGTGACAGCAAGTACA	2388
Qy	773	AlaValAlaValThrValAspLysArgThrAlaIleAlaAlaAlaGlyValGlnMet	792
Db	2389	TCCATCAGCTCCTGGATGAACGAATCTCTGTGGTGGCAGCTGTAGGCATTCAGATG	2448
Qy	793	LysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThrValAsp	812
Db	2449	AAACTTGAATTTTTCCAAAGGAAGTTCTGGACTCCACGACACAGTGTGCTCCCTGGAT	2508
Qy	813	GlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAspAsnAsn	832
Db	2509	GGCAAAATGCTCCATCAGCTGTGATGATGAGACTGTGAATTTGTACCTCATAGACAAATAT	2568
Qy	833	GlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGluValAsp	852
Db	2569	GGATTATTGGTGTCGAAGACTACACAGACTGGAGACTTTTGTGTGAGATCGAG	2628
Qy	853	GlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMetTyrAsp	872
Db	2629	GGAGCTGTGATGAACAAATTCGTAAACATGGGCTCCTTTAAAGAAATACCCCTTTATGAC	2688
Qy	873	TyrGlnAlaMetCysLysProSerSerHisHisSerAlaAlaGlnProLeuValSer	892
Db	2689	TACCAAGCCATGTGTAGGCCAACCAAGGAAGCAGCGATCGCGCCCATGCCCTCTGTGAT	2748
Qy	893	ProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValLeuPheLeu	912
Db	2749	CCATTATATGGCTTCCTCTCTGCAAGTAAATGGATCATGACAGACCTTGCTGTGCTCCTG	2808
Qy	913	LeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSerValPhe	932
Db	2809	GTGGAAATTTAACCTCTGC-----AGTTGTGGCAGCTCCGATATGACAGCTAAAGCC-----	2859
Qy	933	HisHisSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGluTyrPro	952
Db	2860	-----CAGAAATTTGAACACAGACCCCTGGAGCCTGTGTGATATCGAATATCCA	2904
Qy	953	ValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGlyProCys	972
Db	2905	GCATTCTCTCTGAGCCGCCACCATCAAGAGACTACAGGGAATATTCCTGTGAAGACTGC	2964
Qy	973	GlnLysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuValThrAsp	992
Db	2965	TCCAAGTCTTTGTTCATCCAGCAATCCCAAGCAGCAACCTGTTTCATGGTGGTGGTGAC	3024
Qy	993	ProThrCysAspCysSerIlePheProProValLeuGlnGluAlaThrGluValLysTyr	1012
Db	3025	AGCAGCTGCTGTGTGAATCTGTGGCCGCCCATCACCATTGGCAGCCCATTTGAATCAGGTAT	3084

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Qy 1013 AsnAlaSerValIysCysAspArgMetArg 1022
    ||| |||::|||::|||::|||::|||::|||
Db 3085 AATGAATCCCTTAAGTGTGAACGCTCTAAAG 3114

RESULT 6
US-09-397-550-7
; Sequence 7, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCE: 180
; CURRENT APPLICATION NUMBER: US/09/397,550
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 3057
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-397-550-7

Alignment Scores:
Pred. No.: 0 Length: 3057
Score: 3278.50 Matches: 599
Percent Similarity: 78.51% Conservative: 179
Best Local Similarity: 60.44% Mismatches: 200
Query Match: 57.26% Indels: 13
DB: 4 Gaps: 5

US-09-833-222A-10 (1-1090) x US-09-397-550-7 (1-3057)

Qy 13 ValIysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrIysTyrSer 32
Db 124 GTGAAGCTCTGGGCGCTCGGCTTTTGTGGGGAGATAAAATCCATTCTGCTAAGTACTCC 183

Qy 33 GlySerLeuLeuLeuGlnIysIysTyrLysAspValGluSerSerLeuIysIleGluGlu 52
Db 184 GGTTCCAGCTTCTGCANAAGAAATAACAAGAGTATGAGAAGACGCTGCCCATAGAGAA 243

Qy 53 ValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArgArg 72
Db 244 ATTGATGGCTCCCAACTGGTAAGAAGCTGGCAAGACATCGAAGAGATGTTTCACAAG 303

Qy 73 LysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsnHisGlu 92
Db 304 AACTCTGAGCCCTCAGCGCTCTGCTGGAGGCTGCAGAAGAAGCACACCTGAAACATGAA 363

Qy 93 PheAsnGluSerLeuValPheAspTyrTyrAsnSerValIleAsnGluArgaspGlu 112
Db 364 TTTGATGCAGACTTACAGTATGAATACTTCAATGCTGCTGATTAATGAAAGGGGCAAA 423

Qy 113 LysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHisPheSer 132
Db 424 GACGGGAATTTTGGAGCTGGGAAGGAATTCATCTTAGCCCCAATGCACCATTTTAT 483

Qy 133 AsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyrAsnLys 152
Db 484 AATTTCCTGTGAACATCATGCTTAAGTGACGTCGAAGTACCAACGAACATGTACAAACAA 543

Qy 153 AspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPheValGlu 172
Db 544 GACCCCTGCAAATTGTCAATGGGGTTTATTGGTCTGAATCTCTAAACAAGATTTTGTAGAT 603

Qy 173 AsnPheGluArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhePhe 192
Db 604 AACTTTGACCGTGACCCACTCTCATATGGCAGTACTTTGGGAAGTGCAAAGGCGCTTTT 663

Qy 193 ArgIleTyrProGlyIleIysTrpThrProAspGluAsnGlyValIleThrPheAspCys 212
Db 664 AGCAGTATCCGGGGATTAATATGGGAACCAAGATGGAATGGAGTCAATTCGCTTCGACTGC 723

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Qy	213	Arg	Asn	Arg	Gly	Tyr	Phe	Leu	Ala	Ala	Thr	Ser	Pro	Leu	Val	Leu	Val	232	
Db	724	AGG	AAC	CCG	AAA	ATG	TAT	CAT	CAG	GAG	CAAC	TCT	CTC	GAA	AAG	ACG	TGG	TAT	783
Qy	233	Asp	Val	Ser	Gly	Ser	Met	Leu	Gly	Leu	Arg	Met	Thr	Leu	Ala	Val	His	Thr	252
Db	784	GAC	GTG	CAG	TGG	CAG	CAT	GAA	AGG	ACT	CCG	TCT	CGA	CTC	GCG	AAG	CAAC	AGT	843
Qy	253	Ile	Leu	Asp	Thr	Leu	Gly	Glu	Asn	Asp	Phe	Val	Asn	Ile	Leu	Ala	Tyr	Asn	272
Db	844	ATT	TTG	GAT	CAC	TCT	GGG	ATG	TAT	CTT	CAAC	ATA	TGCT	TAT	ATA	TGAG	GAG	CTT	903
Qy	273	His	Tyr	Ile	Glu	Pro	Cys	Phe	Leu	Gly	Ile	Leu	Val	Gln	Ala	Asp	Arg	Asn	292
Db	904	CAC	TAT	GTG	GGA	ACCT	TG	CCT	CAAT	TGGA	ACT	TTG	TG	CAAG	CCG	CAG	CAG	CAAC	963
Qy	293	His	Phe	Leu	Val	Glu	Leu	Met	Val	Leu	Met	Val	Leu	Gly	Val	Gly	Val	Val	312
Db	964	CAC	TTT	CAG	GAG	CAT	CTG	GCA	CAAC	ATTTT	CCG	CAAG	GAAT	TTG	GAAT	TTG	GAAT	TAT	1023
Qy	313	Leu	Arg	Glu	Ala	Phe	Gln	Ile	Leu	Leu	Gln	Phe	Gln	Ile	Ala	Val	Gln	Ser	332
Db	1024	CTG	AAT	GAG	GGC	TTC	CAAC	ATT	TCT	GAG	TGAT	TTT	CAAC	CAC	CGG	GAC	AAG	AGT	1083
Qy	333	Asn	Gln	Ala	Ile	Met	Leu	Ile	Ser	Asp	Gly	Ala	Val	Glu	Asp	Tyr	Glu	Pro	352
Db	1084	AGT	CAG	GC	CA	TGCT	CATA	ACT	TGAT	GCG	GCG	TGG	GAC	ACT	TAT	GAT	ACA	ACT	1143
Qy	353	Lys	Tyr	Asn	Thr	Pro	Asp	Cys	Gly	Val	Arg	Val	Phe	Thr	Tyr	Leu	Ile	Gly	372
Db	1144	AAAT	TACA	AT	TG	CC	CAG	AT	TCG	AAAG	GGT	TG	CGA	TCT	TTC	ACA	ACT	CAT	1203
Qy	373	Ser	Phe	Ala	Asp	Arg	Met	Lys	Tyr	Phe	Ile	Ala	Cys	Asn	Asn	Lys	Gly	Tyr	392
Db	1204	GCG	TTT	GC	AGA	CAAT	CTA	AA	GTG	ATG	GAT	GCG	CTG	CC	CA	AA	AGG	ATTTT	1263
Qy	393	Ser	Thr	Leu	Ala	Asp	Thr	Gln	Glu	Asn	Val	Met	Glu	Tyr	Leu	His	Val	Leu	412
Db	1264	TCC	ACC	TTG	CGT	GTG	TGC	CAG	GAA	TGT	CA	TG	GAAT	TAC	CTT	CAG	TGCT	TAG	1323
Qy	413	Met	Val	Ile	Asn	His	Asp	His	Asp	Ile	Leu	Thr	Glu	Ala	Tyr	Met	Asp	Ser	432
Db	1324	AAAG	TCA	T	CG	AC	GAG	GAT	GAT	GTG	TG	TG	CG	CA	AG	CTT	TAC	AT	1383
Qy	433	Leu	Ser	Ser	Gln	Ala	Gln	Ser	Leu	Thr	Leu	Thr	Thr	Val	Ala	Met	Pro	Val	452
Db	1384	ACT	GAT	GAT	CAT	CAG	GGC	CCC	-----	GT	CT	GT	AT	GAT	ACC	ATG	TAG	CGC	1437
Qy	453	Lys	Leu	Asn	Glu	Thr	Arg	Ser	His	Gly	Ile	Leu	Gly	Val	Val	Gly	Ser	Asp	472
Db	1438	AAG	CAG	AAC	GGA	CAAC	GAT	CGA	AGG	CAT	TCT	CTG	GGG	ATG	TG	TG	GCA	CAG	1497
Qy	473	Leu	Arg	Glu	Leu	Met	Lys	Leu	Ala	Pro	Arg	Tyr	Lys	Leu	Gly	Val	His	Gly	492
Db	1498	GTG	AAAG	AAC	CTT	CT	GAA	GAC	CACT	CCCC	AAAA	TACA	AGT	TAG	GGAT	TTC	ACG	GGT	1557
Qy	493	Leu	Asn	Thr	Asn	Asn	Gly	Tyr	Ile	Leu	Ser	His	Pro	Asp	Leu	Arg	Pro	Leu	512
Db	1558	GCA	AT	CA	CAA	TAAT	TG	GTAT	TAT	CCT	GAC	GCAT	CCG	GAAC	T	CAG	CGCT		

Qy	573	PhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArgGlyHis	592
Db	1795	TATTATACAGACATCAAGGGTACTCTCTTTTCAGTTTAGTGTGGCGCTTTTCCAGAGGTCAAT	1854
Qy	593	GlyGluTrpIleLeuLeuGlyAenThrSerValGluGluGluGlyLeuHisAspLeuLeuHis	612
Db	1855	GGGAATATTTCTTCCGAGGGAATGTACCATCGAAGAAGCCCTGCATGACTTAGAACAT	1914
Qy	613	ProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspProAspHis	632
Db	1915	CCCGATGTCTTGGCAGATGAATGGTCTACTCTCAACACACTGACCTACACCCCTGAGCAC	1974
Qy	633	ArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspProAspLeu	652
Db	1975	CGCCATCTGTCTCAGTTTAGAAGCGAATTAAGCTCTACTATAAAGCGCAAGAACCTCTGCTC	2034
Qy	653	GluCysAspGluGluLeuValArgGluValLeuPheAspAlaValValThrAlaProMet	672
Db	2035	CAGTGTGATTAAGAATTGATCCAAAGAAGTCTTTTTTGACCGGCTGGTGTAGTGCCCCCATY	2094
Qy	673	GluAlaTrpTrpThrAlaLeuAlaLeuAenMetSerGluGluSerGluHisValValAsp	692
Db	2095	GAAGCGATTGGACGACCTGGCCCTCAACAATCTGAAATTTCTGACAGGCGGTGGAG	2154
Qy	693	MetAlaPheLeuGlyThrArgAlaGlyLeuLeuAArgSerSerLeuPheValGlySerGlu	712
Db	2155	GTTGCCCTTCTCGCACTCGCACGGGCTCTCCAGAATCAACCTGTTGTGTGGGGCTGAG	2214
Qy	713	LysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThrLeuAsp	732
Db	2215	CAGCTCACCAATCAGGACTTCTCGAAAGCTGGCGCAAGAGAACAATTTTAAACGGCAGAC	2274
Qy	733	ArgPheProLeuTrpTrpArgGlnAlaSerGluHisProAlaGlySerPheValPheAsn	752
Db	2275	CATTTCCTCTCTGTACCAAGAGCGGTGACAGACTCCAGGGAGCTTCGTCTACTCG	2334
Qy	753	LeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAlaSerThr	772
Db	2335	ATCCCAATTCAGCACTGGACCA-----GTCAATAAAAGCAATCTGGTGCAGCAAGTACA	2388
Qy	773	AlaValAlaValThrValAspLysArgThrAlaIleAlaAlaAlaGlyValGlnMet	792
Db	2389	TCCATCCAGCTCTGGATGAACGGAAATCTCTGTGTGGCAGCTGTAGGCATTCAGATG	2448
Qy	793	LysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThrValAsp	812
Db	2449	AAACTTGAAATTTTCCAAAGAAAGTCTGGAGTCCAGCAGACAGCTGCTGCTCCCTGGAT	2508
Qy	813	GlyProTrpThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAspAenAen	832
Db	2509	GGCAATATGCTCCATCAGCTGTGTATGATGAGACTGTGAAATTTGTACCTCATAGACAATAAT	2568
Qy	833	GlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGluValAsp	852
Db	2569	GGATTTATTTTGGTGTCTGAAGACTACACAGACTGGAGACTTTTTTGGTGAGATCGAG	2628
Qy	853	GlyValAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMetTyrAsp	872
Db	2629	GGAGCTGTGATGAACAAATTTGCTAACAAATGGGCTCTCTTAAAGAAATTAACCTTTATGAC	2688
Qy	873	TyrGlnAlaMetCysLysProSerSerHisHisSerAlaAlaGlnProLeuValSer	892
Db	2689	TACCAAGCCATGTGTAGAGCCAAACAGGAAGACGCGATGGCGCCCATCGCTCTCTGGAT	2748
Qy	893	ProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValLeuPheLeu	912
Db	2749	CCTTATAATGCCCTCTCTCTCGCAGTAAAAATGGATCATGACAGAACTGTCTGTGTTCTCG	2808
Qy	913	LeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSerValPhe	932
Db	2809	GTGGAATTTAACTCTGCG-----AGTGTGGTGCATCTCCGATATGACAGCACTAAAGCC-----	2859
Qy	933	HisHisSerHisLysHisLysLysGlnAspProProLeuGlnProCysAspThrGluTrpPro	952

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Db 2860 -----CAGAAATTGAAACACAGACCCCTGGAGCTTGTGATACCTGAATATCCA 2904
Qy 953 valPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGlyProCys 972
Db 2905 GCATTCTCTCTGAGCGCACCATCATCAGGAGACTACAGGGAATATTGCTTGTGAAGACTGC 2964
Qy 973 GlnLysValPheValGlnGlnIleProAsnSerAsnLeuLeuLeuLeuValThrAsp 992
Db 2965 TCCAGTCCCTTGTGATCCAGCAAAATCCAGCAGCAACCTGTTTCATGGTGGTGGTGAC 3024
Qy 993 ProThrCysAspCysSerIlePheProVal 1003
Db 3025 AGCAGCTGCCTCTGTGAATCTGTGGCCCCCATC 3057

RESULT 7
US-09-397-550-15
; Sequence 15, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCE: 180
; CURRENT APPLICATION NUMBER: US/09/397,550
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 15
; LENGTH: 1050
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-397-550-15

Alignment Scores:
Pred. No.: 4,77e-195 Length: 1050
Score: 1792.50 Matches: 341
Percent Similarity: 98.00% Conservative: 2
Best Local Similarity: 97.43% Mismatches: 6
Query Match: 31.30% Indels: 1
DB: 4 Gaps: 1

US-09-833-222A-10 (1-1090) x US-09-397-550-15 (1-1050)

Qy 700 AlaGlyLeuLeuArgSerSerLeuPheValGlySerGluLysValSerAspArgLysPhe 719
Db 1 AGTGCCCTCTCGAAGCAGCTTGTTCGTGGGCTCCGAGAAGTCTCCGACAGGAAGTTC 60
Qy 720 LeuThrProGluAspGluAlaSerValPheThrLeuAspArgPheProLeuTyrTyrArg 739
Db 61 CTGACACCTGAGACGCGGCGCAGCGTGTTCACCTCTGGACCGCTTCGCGTGTGTAACCGC 120
Qy 740 GlnAlaSerGluHisProAlaGlySerPheValPheAsnLeuArgTrpAlaGluGlyPro 759
Db 121 CAGGCTCTCAGAGCATCTGCTGCGCAGCTTCTTCAACCTCCGCTGGGCGAGAAGACCA 180
Qy 760 GluSerAlaGlyGluProMetValValThrAlaSerThrAlaValAlaValThrValAsp 779
Db 181 GAAAGTGGGGGTGAACCCATGTGGTGGTGACGCGCAAGCACAGCTGTGGCGGTGACCGTGAC 240
Qy 780 LysArgThrAlaIleAlaAlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArg 799
Db 241 AAGAGACACCAATTGCTGACGCGCGGGGCTCAAAATGAAGCTGAATTCCTCCAGCGC 300
Qy 800 LysPheTrpAlaAlaThrArgGlnCysSerThrValAspGlyProTyrThrGlnSerCys 819
Db 301 AAATTCTGGCGCGCAACGCGCAGTGCAGCACTGTGATGGGCGGTGCACACAGAGCTGC 360
Qy 820 GluAspSerAspLeuAspCysPheValIleAspAsnGlyPheIleLeuIleSerLys 839
Db 361 GAGGACAGTGATCTGACTGCTTCTCGTATCCGACCAACAGGGTTCATTCTGATCTCCAAG 420
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Qy 840 ArgSerArgGluThrGlyArgPheLeuGlyGluValAspGlyAlaValLeuThrGlnLeu 859
Db 421 AGTCCCGAGAGACGGAAGATTCTGGGGAGGTGGATGGTCTGCTCTGACCCAGCTG 480
Qy 860 LeuSerMetGlyValPheSerGlnValThrMetTyrAspTyrGlnAlaMetCysLysPro 879
Db 481 CTCAGCATGGGGGTGTTTTCAGCCAAAGTGACTATGTATGACTATCAGGCCATGTCAAACCC 540
Qy 880 SerSerHisHisSerAlaAlaGlnProLeuValSerProIleSerAlaPheLeuThr 899
Db 541 TCGAGTCACACACACAGTGCAGCCAGCCCTGGTCAGCCCAATTTCTGCCCTTCTTGACG 600
Qy 900 AlaThrArgTrpLeuLeuGlnGluLeuValLeuPheLeuLeuGluTyrPheValTyrGly 919
Db 601 GCGACCAAGTGTGCTGCTGAGGAGCTGGTGTCTTCTGCTGGAGTGGAGTGTCTGGGGC 660
Qy 920 SerTrpTyrAspArgGlyAlaGluAlaLysSerValPheHisSerHisLysHisLys 939
Db 661 TCTGTGTACGACAGAGGGCGGAGGCAAAAGTGTCTTCCATCCTCCCAACACACAAG 720
Qy 940 LysGlnAspProLeuGlnProCysAspThrGluTyrProValPheValTyrGlnProAla 959
Db 721 AAGCAGGACCCCTGCGAGCCCTGCGACGCGAGTACCCCGTGTCTGTGTACCGCGGCC 780
Qy 960 IleArgGluAlaAsnGlyIleValGluCysGlyProCysGlnLysValPheValValGln 979
Db 781 ATCCGGGAGGCCAACCGGATCTGTGGAGTGGGGCCCTGCCAGAGGATATTGTGTGTCAG 840
Qy 980 GlnIleProAsnSerAsnLeuLeuLeuValThrAspProThrCysAspCysSerIle 999
Db 841 CAGATTCCCAACAGTAACCTCTCTCTCTGTCGACAGAGCCACCTGTGACTGCAGCATC 900
Qy 1000 PheProProValLeuGlnGluAlaThrGluValLysTyrAsnAlaSerValLysCysAsp 1019
Db 901 TTCCACCACTGCTGCGAGGCGCAGAAAGTCAAAATATAATGCCTCTCTCAAAATGTGAC 960
Qy 1020 ArgMetArgSerGlnLysLeuArgArgProAspSerCysHisAlaPheHisProGlu 1039
Db 961 CGGATGCGCTCCAGAGAGTCCGCGCGGCGACAGACTCTCTGCGACGCCCTTCCATCCAGAG 1020
Qy 1040 ValArgValGluAlaAspArgGlyTrpAla 1049
Db 1021 GAGAAATGCCAG---GACTGCGGCGGCGCC 1047

RESULT 8
US-09-397-550-14
; Sequence 14, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCE: 180
; CURRENT APPLICATION NUMBER: US/09/397,550
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 14
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-397-550-14

Alignment Scores:
Pred. No.: 6,27e-184 Length: 969
Score: 1695.00 Matches: 321
Percent Similarity: 99.69% Conservative: 1
Best Local Similarity: 99.38% Mismatches: 1
Query Match: 29.60% Indels: 0
DB: 4 Gaps: 0

US-09-833-222A-10 (1-1090) x US-09-397-550-14 (1-969)
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Qy 700 AlaGlyLeuLeuArgSerSerLeuPheValGlySerGluLysValSerAspArgLysPhe 719
Db 1 AGTGGCTCTCTGAGAAGCAGCTGTTGCTGGCTCCGAGAGGTCTCCGACAGGAAGTTC 60
Qy 720 LeuThrProGluAspGluAlaSerValPheThrLeuAspArgPheProLeuTyrPheArg 739
Db 61 CTGACACCTGAGGACGAGGCGAGCGTGTTCACCTCGGACCGCTTCCGCGTGTGGTACCGC 120
Qy 740 GlnAlaSerGluHisProAlaGlySerPheValPheAsnLeuArgTTPAlaGluGlyPro 759
Db 121 CAGGCTCAGAGCATCTCTGTCGAGCTTCTTCAACCTCGCTGGGCGAGAGNACCA 180
Qy 760 GluSerAlaGlyGluProMetValThrAlaSerThrAlaValAlaValThrValAsp 779
Db 181 GAAAGTGGGCTGAACCATGGTGTGACGCAAGCACAGCTGTGGCGGTGACCGTGGAC 240
Qy 780 LysArgThrAlaIleAlaAlaAlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArg 799
Db 241 AAGAGGACAGCCATTGCTGACGCGCGGCGTCCAAATGAAGCTGGAAATTCCTCCAGCGC 300
Qy 800 LysPheTTPAlaAlaThrArgGlnCysSerThrValAspGlyProTyrThrGlnSerCys 819
Db 301 AAATTCTGGCGGCAACCGCGCAGTGCAGCAGCTGTGATGGCGGTGCACACAGAGTGC 360
Qy 820 GluAspSerAspLeuAspCysPheValIleAspAsnAsnGlyPheIleLeuIleSerLys 839
Db 361 GAGGACAGTATCTGGACTGCTTCGTCTATCGACAAACAGGGTTCATTCTGATCTCCAAG 420
Qy 840 ArgSerArgGluThrGlyArgPheLeuGlyGluValAspGlyAlaValLeuThrGlnLeu 859
Db 421 AGGTCCCGAGAGACGGGAAGATTTCTGGGGAGGTGATGGTGTCTGTCCTGACCCAGCTG 480
Qy 860 LeuSerMetGlyValPheSerGlnValThrMetTyrAspTyrGlnAlaMetCysLysPro 879
Db 481 CTGAGCATGGGGTGTTCAGCCCAAGTGAATATGATATGACTATCAGGCCATGTGCNAACCC 540
Qy 880 SerSerHisHisSerAlaAlaGlnProLeuValSerProIleSerAlaPheLeuThr 899
Db 541 TCAGTCAACCAACACAGCTGCAGCCAGCCCTGTGTGACGCCAATTTCTGCTTCTTGACG 600
Qy 900 AlaThrArgTTPLeuLeuGlnLeuValLeuPheLeuLeuGluTTPSerValTTPGly 919
Db 601 GCGACCAAGTGGTGTCTGACGAGCTGGTGTCTTCTGCTGGAGTGGAGTGTCTGGGGC 660
Qy 920 SerTTPArgArgGlyAlaGluAlaLysSerValPheHisHisSerHisLysHisLys 939
Db 661 TCTGTGTACACAGAGGGGCGAGGCCCAAAAGTGTCTTCCATCCTCCCAACACACAG 720
Qy 940 LysGlnAspProLeuGlnProCysAspThrGluTyrProValPheValTyrGlnProAla 959
Db 721 AAGCAGGACCGCTGCAGCCCTGCGACACAGGAGTACCCCGTTCGTGTGACCGCGCC 780
Qy 960 IleArgGluAlaAsnGlyIleValGluCysGlyProCysGlnLysValPheValGln 979
Db 781 ATCCGGAGAGCAACCGGGATCGTGGAGTGGCGGCCCTGCCAGAGGATTTGTGGTGCAG 840
Qy 980 GlnIleProAsnSerAsnLeuLeuLeuValThrAspProThrCysAspCysSerIle 999
Db 841 CAGATTCCTCAACAGTAACCTCTCTCTGCTGGTGCAGACCCACCTGTGTGACGAGATC 900
Qy 1000 PheProValLeuGlnGluAlaThrGluValLysTyrAsnAlaSerValLysCysAsp 1019
Db 901 TTCCACCAAGTGTCTGAGGAGGCGACAGAGTCAAATATAATGCTCTGTCAAATGTGAC 960
Qy 1020 ArgMetArg 1022
Db 961 CGGATGGCG 969
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RESULT 9

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US-09-397-550-13
; Sequence 13, Application US/09397550
; Patent No. 678952
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; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCES: 180
; CURRENT APPLICATION NUMBER: US/09/397,550
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 912
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-397-550-13
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Alignment Scores:

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Pred. No.: 7,47e-173 Length: 912
Score: 1598.00 Matches: 302
Percent Similarity: 99.67% Conservative: 1
Best Local Similarity: 99.34% Mismatches: 1
Query Match: 27.91% Indels: 0
DB: 4 Gaps: 0
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US-09-833-222a-10 (1-1090) x US-09-397-550-13 (1-912)

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Qy 700 AlaGlyLeuLeuArgSerSerLeuPheValGlySerGluLysValSerAspArgLysPhe 719
Db 1 AGTGGCTCTCTGAGAAGCAGCTTGTTCGTGGCTCCGAGAGGTCTCCGACAGGAAGTTC 60
Qy 720 LeuThrProGluAspGluAlaSerValPheThrLeuAspArgPheProLeuTyrPheArg 739
Db 61 CTGACACCTGAGGACGAGGCGAGCGTGTTCACCTCGGACCGCTTCCGCGTGTGGTACCGC 120
Qy 740 GlnAlaSerGluHisProAlaGlySerPheValPheAsnLeuArgTTPAlaGluGlyPro 759
Db 121 CAGGCTCAGAGCATCTCTGTCGAGCTTCTTCAACCTCGCTGGGCGAGAGNACCA 180
Qy 760 GluSerAlaGlyGluProMetValThrAlaSerThrAlaValAlaValThrValAsp 779
Db 181 GAAAGTGGGCTGAACCATGGTGTGACGCAAGCACAGCTGTGGCGGTGACCGTGGAC 240
Qy 780 LysArgThrAlaIleAlaAlaAlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArg 799
Db 241 AAGAGGACAGCCATTGCTGACGCGCGGCGTCCAAATGAAGCTGGAAATTCCTCCAGCGC 300
Qy 800 LysPheTTPAlaAlaThrArgGlnCysSerThrValAspGlyProTyrThrGlnSerCys 819
Db 301 AAATTCTGGCGGCAACCGCGCAGTGCAGCAGCTGTGATGGCGGTGCACACAGAGTGC 360
Qy 820 GluAspSerAspLeuAspCysPheValIleAspAsnAsnGlyPheIleLeuIleSerLys 839
Db 361 GAGGACAGTATCTGGACTGCTTCGTCTATCGACAAACAGGGTTCATTCTGATCTCCAAG 420
Qy 840 ArgSerArgGluThrGlyArgPheLeuGlyGluValAspGlyAlaValLeuThrGlnLeu 859
Db 421 AGGTCCCGAGAGACGGGAAGATTTCTGGGGAGGTGATGGTGTCTGTCCTGACCCAGCTG 480
Qy 860 LeuSerMetGlyValPheSerGlnValThrMetTyrAspTyrGlnAlaMetCysLysPro 879
Db 481 CTGAGCATGGGGTGTTCAGCCCAAGTGAATATGATATGACTATCAGGCCATGTGCNAACCC 540
Qy 880 SerSerHisHisSerAlaAlaGlnProLeuValSerProIleSerAlaPheLeuThr 899
Db 541 TCAGTCAACCAACACAGCTGCAGCCAGCCCTGTGTGACGCCAATTTCTGCTTCTTGACG 600
Qy 900 AlaThrArgTTPLeuLeuGlnLeuValLeuPheLeuLeuGluTTPSerValTTPGly 919
Db 601 GCGACCAAGTGGTGTCTGACGAGCTGGTGTCTTCTGCTGGAGTGGAGTGTCTGGGGC 660
Qy 920 SerTTPArgArgGlyAlaGluAlaLysSerValPheHisHisSerHisLysHisLys 939
Db 661 TCTGTGTACACAGAGGGGCGAGGCCCAAAAGTGTCTTCCATCCTCCCAACACACAG 720
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QY 940 LysGlnAspProLeuGlnProCysAspThrGluTyrProValPheValTyrGlnProAla 959
Db 721 AAGCAGACCCGCTGACAGCCTCGGACACGAGTACCCCGTTCGTTACCAAGCCGCGC 780
QY 960 IleArgGluAlaAsnGlyIleValGluCysGlyProCysGlnLysValPheValValGln 979
Db 781 ATCCGGAGGCCAACCGGATCGTGGAGTGGCGGCCCTGCCAGAAAGTATTGTTGGTGCAG 840
QY 980 GlnIleProAsnSerAsnLeuLeuLeuLeuValThrAspProThrCysAspCysSerIle 999
Db 841 CAGATTCCCAACAGTAACCTCCTCCTCGTGTGACAGACCCACCTGTGTGATCGAGCATC 900
QY 1000 PheProProVal 1003
Db 901 TTCCCAACAGTG 912

RESULT 10
US-09-470-443-5
; Sequence 5, Application US/09470443
; Patent No. 6441156
; GENERAL INFORMATION:
; APPLICANT: Lerman, Michael I.
; APPLICANT: Minna, John D.
; APPLICANT: Latif, Farida
; APPLICANT: Wei, Ming-Hui
; APPLICANT: Sekido, Yoshitaka
; APPLICANT: Gao, Boning
; APPLICANT: Duh, Fuh-Mei
; TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof
; FILE REFERENCES: NIH-05043
; CURRENT APPLICATION NUMBER: US/09/470,443
; CURRENT FILING DATE: 1999-12-22
; EARLIER APPLICATION NUMBER: 60/114,359
; EARLIER FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 5279
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (185)..(3415)
US-09-470-443-5

Alignment Scores:
Pred. No.: 1.63e-124 Length: 5279
Score: 1188.50 Matches: 349
Percent Similarity: 47.61% Conservative: 208
Best Local Similarity: 29.83% Mismatches: 432
Query Match: 20.76% Indels: 181
DB: 3 Gaps: 44

US-09-833-222A-10 (1-1090) x US-09-470-443-5 (1-5279)
QY 10 ArgAspArgValLysLeuTyrAlaAspThrPheGlyAspLeuTyrAsnThrValThr 29
Db 176 CCGGGCGTGTAGCAGCAGCTCGGCGCGCGCGTCTGGAGCAGGAGGTGCAGCGCGGTGCGG 235
QY 30 LysTyr-SerGlySerLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLys 49
Db 236 ATTTTGGAGCGCTCCAGCAGCTCCGTGAGATTTCAGAGCAACCGGAACCTGTTCCGAG 295
QY 50 IleGluGluValAspGlyLeuLeuValArgLysPheSerGluAspMetGluAsnMet 69
Db 296 GTACAGGAGAATGAGCCTCAGAAAGTTGGTGGAGAGGTGGCAGGGGACATTGAGAGCCTT 355
QY 70 LeuArgArgLysValGluAlaValGlnAsnLeuValGluAlaGluAlaAspLeu 89
Db 356 CTGCACAGGAGGTGACGGCCCTGAGAGACTGGTGTGCTGCAGAGAACTTCCAGAA 415
QY 90 AsnHisGluPheAsnGluSerLeuValPheAsp-----TyrTyrAsnSerValLeu 106
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Db 416 GCACACCGCTGGCAGACACATCAAGGAGGAGACATCGTGTACTATGACGCCAAGGCT 475
QY 107 IleAsnGluArgAspGlu---LysGlyAsnPheValGluLeuGlyAla----- 121
Db 476 GACGCTGAGCTGACGACCGCTGAGAGTGTGAAAGGGGGTCTAAGGCGCAGCACCC 535
QY 122 -----GluPheLeuLeuGluSerAsnAlaHisPheSerAsnLeuProValAsnThr 138
Db 536 CTAAAGGCTCGACTTTCATCGAGGACCCCAAC-----TTCAAGAAC---AAGGTCAACTAT 586
QY 139 SerIleSerValGlnLeuProThrAsnValTyrAsnLysAspProAspIleLeuAsn 158
Db 587 TCATACGCGGCTGTACAGATCCCTACGACATCTACAAAGGCTCCACTGTCTCATCTCAAT 646
QY 159 GlyValTyrMetSerGluAlaLeuAsnAlaValPheValGluAsnPheGlnArgAspPro 178
Db 647 GAGCTCAACTGGACAGAGGCCCTTGGAGAATGTTCATGGAAACCCGACAGACACCC 706
QY 179 ThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhePheArgIleTyrProGlyIle 198
Db 707 ACATCTGTGTGGAGTCTTTCGGCAGCGCCACAGGAGTCACTCGCTACTACCCGGCCACC 766
QY 199 LysTrpThrProAspGluAsnGlyValIleThrPheAspCysArgAsnArgGlyTyrTyr 218
Db 767 CCGTGGCGAGCCCCCAAGAAG---ATCGACCTGTACGATGTCCGAGGAGACCCCTGGTAT 823
QY 219 IleGlnAlaAlaThrSerProLysAspIleValIleLeuValAspValSerGlySerMet 238
Db 824 ATCCAGGGGGCCCTCGTCACCCAAAGACATGTGTCATCTGTGGATGTGAGTGGCAGTGTG 883
QY 239 LysGlyLeuArgMetThrIleAlaLysHisThrIleThrThrIleLeuAspThrLeuGly 258
Db 884 ACGGCGCTGACCTGAAGCTGATGAAGACATCTGTCTCGAGAGTGTGACACGCTGTCT 943
QY 259 GluAsnAspPheValAsnIleAlaTyrAsnAspTyrValHisTyrIleGluProCys 278
Db 944 GATGATGACTATGTGAATGTGGCTCGTTCACGAGAGGACAGCAGCTGTGTCA---TGC 1000
QY 279 PheLysGlyIleLeuValGlnAlaAspArgAspAsnArgGluHisPheLysLeuVal 298
Db 1001 TTCACACAC---CTGGTGCAGGCCCAATGTGCGCAACAAGAAGGTGTTCAGGAGAGTGTG 1057
QY 299 GluGluLeuMetValLysGlyValGlyValValAspGlnAlaLeuArgGluAlaPheGln 318
Db 1058 CAGGGCATGTGGCCCAAGGGCACAGGCTACAAGCGCGCTTTCAGTATGCTTGTGAC 1117
QY 319 IleLeuLysGlnPheGlnGluAlaLysGlnGlySerLeuCysAsnGlnAlaIleMetLeu 338
Db 1118 CAGCTGCAGAACTCCCAACATCACTCGGGCCAAC-----TGCAACAAGATGATCATGATG 1171
QY 339 IleSerAspGlyAlaValGluAspTyrGluProValPheGluLysTyrAsnTyrProAsp 358
Db 1172 TTCACGGATGGTGGTGGAGGACCGCGTGCAGGACGCTCTTTTGAGAAGTACAAATGGCCCAAAC 1231
QY 359 CysLysValArgValPheThrTyrLeuIleGlyArgGluValSerPheAlaAspArgMet 378
Db 1232 CGACCGTCCGCGTGTTHACTTCTCCGTTGGGGCAGCATAACTATGACGTACACCGCTG 1291
QY 379 LysTrpIleAlaCysAsnAsnLysGlyTyrTyrThrGlnIleSerThrLeuAlaAspThr 398
Db 1292 CAGTGGATGGCTGTGCCAACAAAGGCTACTATTTTGAGATCCCTTCCATCGGAGCATC 1351
QY 399 GlnGluAsnValMetGluTyrLeuHisValLeuSerArgProMetValIle-----Asn 416
Db 1352 CGCATCAACACACAGGAATATCTAGATGTGTGGGCGAGCCCATGTGTGTGGCAGGCAAG 1411
QY 417 HisAspHisAspIleIleTrpThrGluAlaTyrMetAspSerLysLeuLeuSerSerGln 436
Db 1412 GAGGCCACAGGTTTCAGTGGACCAACGCTGTATGAGAT----- 1450
QY 437 AlaGlnSerLeuThrLeuLeuThrThrValAlaMetProValPheSer----- 452
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Db 1451 GCACTGGGACTGGGGTGGTGAACAGGGACCTCCCTGTTTCAACCTGCACACAGGAT 1510
Qy 453 -----LysLysAsnGluThrArgSerHisGlyLeuLeuGlyValValGly 468
Db 1511 GGCCCTGGGAAAGAAAGAACCCAG-----CTGATCCTGGGGTGTATGGCC 1555
Qy 469 SerAspValAlaLeuArgGluMetLysLeuAlaProArgTyrLysLeuGlyValHis 488
Db 1556 ATTGACGTGCTCTGAATGACATCAAGAGGCTGACCCCACTACACGCTGGAGCCAAAC 1615
Qy 489 GlyTyrAlaPheLeuAnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgPro 508
Db 1616 GGCTATGTTGGCATTTGACCTGAACCGGTACGTGTGTGTCACCCCAATCTCAAGCCC 1675
Qy 509 Leu-----TyrArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerVal 525
Db 1676 CAGACCACCAACTTCCGGGAGCCTGTGACTCTG----- 1708
Qy 526 AspLeuSerGluValGluTrpGluAspGln---AlaGluSerLeuArgThrAlaMetIle 544
Db 1709 GACTTCTGATCGGAGCTAGAGATGAGAAAGAGAGATCCGTCGGAGCATGATT 1768
Qy 545 AsnArgGluThrGlyThrLeuSerMetAspValLysValProMetAspLysGlyLysArg 564
Db 1769 GATGGCAACAGGGCCCAACAGCAGATCAGAACGTTGTGTCAGTCCCTGGATGAGAGGTAC 1828
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Qy 585 GlyAlaValLeuSerArgGlyHisGlyGluTyrIle----- 596
Db 1889 GGGCTGTGTCCCACTCAGCAGCCTTCTACCTCCAAGCCAACTCTCAGTGACCAGATC 1948
Qy 597 -----LeuLeuGlyAsnThrSerValGluGluGlyLeuHis 608
Db 1949 CTCAGGTCAAGTATTTAGTTCCTGCTCCCGAGCTTTGAGTCTGAAGGA---CAC 2005
Qy 609 AspLeuLeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIle 628
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Qy 629 AspProAspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLys 648
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Qy 649 AspProAsp---LeuGluCysAspGluLeuValargGluValLeuPheAspAlaVal 667
Db 2102 ACTCCAGACTCCAAGCAGTGCACAACCTTCTCTGCACAACTGATCTTGGACACGGGC 2161
Qy 668 ValThrAlaProMet---GluAlaTyrTriphThrAlaLeuAlaLeuAsnMetSerGluGlu 686
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Qy 687 SerGluHisValValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSer 706
Db 2210 ---ACGTACAGCTACTGGCGCTGTCGTCGCACACAGCGGTGGCATCACCCGA----- 2260
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Db 2261 -----GTCCTCCCAACAAGGCAGCT 2281
Qy 727 SerValPheThrLeuAspArgPheProLeu-----TrpTyrArgGlnAlaSerGlu 743
Db 2282 GAGGACTGGACAGAGAACCCCTGAGCCCTTCAATGCCAGCTTCTACCGCCGAGCCTGGAT 2341
Qy 744 HisProAlaGlySerPheValPheAsn-----LeuArgTrpAla 756
Db 2342 AAC-----CACGTTATGTCTTCAAGCCCCCACCAGGATGCCCTGTTAAGG----- 2389
Qy 757 GluGlyPro---GluSerAlaGlyGluProMetValThrAlaSerThrAlaValAla 775
Db 2390 -----CCGCTGGAGCTGGAGAATGACACTGTGGGCATCTCTCGTCAGCAGCTGTGGAG 2443

Qy 776 ValThrValAspLysArgThrAlaIleAlaAlaAlaAlaGlyValGlnMetLysLeuGlu 795
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Qy 796 PheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThrValAspGlyProTyr 815
Db 2504 GCTTGGGCTGAGAAGTTTCAAGGTGTAGCCAGCAACGTTACCCACCAAGACCACT--- 2560
Qy 816 ThrGlnSerCys-----GluAspSerAsp 823
Db 2561 ---CAGAGTTCGGGCCCAACAGCCACTGTGAGATGAGCTGCGAGGTTTAACAATGAGGAC 2617
Qy 824 LeuAspCysPheValIleAspAsnAsnGlyPheIleLeuIleSerLysArgSerArg--- 842
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Qy 843 -----GluThrGlyArgPheLeuGlyGluValAspGlyAlaValLeuThrGlnLeu 860
Db 2678 TGGGACCCAGGTGGCGAGTTCTTCAGTGGGTGGATGCCAACCTGTGCTGGCACTCTAC 2737
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Qy 881 SerHisHisSerAlaAlaGlnPro-----LeuValSerProIleSerAlaPhe 897
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Db 2858 CTTAACTGCGCTGTGGAGACTCTGTGCGCCCTGTGCTCTTCCAGAGACTCTCTAC 2917
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Db 2918 GGCTC-----ATCTACACAGCTGTGTTCCAACGACAGCCCCGCGGAGCCGAGGG 2968
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Qy 949 ThrGluTyrProValPheValTyrGlnProAlaIleArgGluAla---AsnGlyIleVal 967
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Qy 968 GluCysGlyProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLeuLeu 987
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Qy 1007 AlaThrGluValLysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeu 1026
Db 3176 GAGACGCACTCCCGCAGCGGACCGCGAGCTGTAGTAGTGTGAGACACCGGATAC 3235
Qy 1027 ArgArgArgProAspSerCysHisAlaPheHis---ProGluValArgValGluAlaAsp 1045
Db 3236 CGGAGAGCGCCGCACATCTGCTTCGACTACACCGCAGACAGATACCTCAGACTGTGGC 3295
Qy 1046 ArgGlyTrpAlaGlyPhe-----SerSerProAsnProLeu 1057
Db 3296 CGCGGG---GCCCTCTTCCCGCGCTCGCTGGGGGTCTCTGGTCTCTCCCTGCACTGCTGCTC 3352
Qy 1058 CysLeuGlyLeuCysProCysArgGlnGluHisIleGlyMet----- 1071
Db 3353 CTCTGGGCTGCGCGCCCGCGCGCAGCTCAAGTCTCTCCAGCGCTCTCGCGCGCTC 3412
Qy 1072 -----ProMetAsnThrProValProVal 1079
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RESULT 11

US-09-470-443-1
; Sequence 1, Application US/09470443
; Patent No. 6441156
; GENERAL INFORMATION:
; APPLICANT: Lerman, Michael I.
; APPLICANT: Minna, John D.
; APPLICANT: Latif, Farida
; APPLICANT: Wei, Ming-Hui
; APPLICANT: Sekido, Yoshitaka
; APPLICANT: Gao, Boning
; APPLICANT: Duh, Fun-Wei
; TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof
; FILE REFERENCE: NIH-05043
; CURRENT APPLICATION NUMBER: US/09/470,443
; CURRENT FILING DATE: 1999-12-22
; EARLIER APPLICATION NUMBER: 60/114,359
; EARLIER FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 5463
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (162)..(3599)
US-09-470-443-1

Alignment Scores:

Pred. No.: 2,26e-124 Length: 5463
Score: 1187.50 Matches: 348
Percent Similarity: 47.59% Conservative: 206
Best Local Similarity: 29.90% Mismatches: 429
Query Match: 20.74% Indels: 181
DB: 3 Gaps: 44

US-09-833-222A-10 (1-1090) x US-09-470-443-1 (1-5463)

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QY 36 LeuLeuGlnLysTyrLysAspValGluSerSerLeuLysIleGluGluValAspGly 55
DB 438 CAGCTCGTCGATTTACAGGACACCCGGAACCTGTTCCAGGTACAGGAGATGAGCCT 497
QY 56 LeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArgArgLysValGlu 75
DB 498 CAGAAGTTGGTGAGAGAGGTGGCAGGGGACATTGAGAGCCCTTCTGGACAGGAAGGTGCAG 557
QY 76 AlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsnHisGluPheAsnGlu 95
DB 558 GCCTGNAGAGATGGCTGTATGTCAGAGAACTTCCAGAAACACACCCGCTGGCAGGAC 617
QY 96 SerLeuValPheAsp-----TyrTyrAsnSerValLeuIleAsnGluArgAspGlu 112
DB 618 AACATCAAGGAGGAGACATCGTGTACTATGACCCCAAGGCTGACGCTGAGCTGGAGCAG 677
QY 113 ---LysGlyAsnPheValGluLeuGlyAla-----GluPheLeu 124
DB 678 CCTGAGAGTGGAGTGGGAAAGGGGCTCTAAGGCCAGCACCCCTAAGGCTGGACTTCATC 737
QY 125 LeuGluSerAsnAlaHisPheSerAsnLeuProValAsnThrSerIleSerSerValGln 144
DB 738 GAGGACCCCAAC-----TTCAAGAAC---AAGGTCACTATTTCATACGGCGCTGTACAG 788
QY 145 LeuProThrAsnValTyrAsnLysAspProAspIleLeuAsnGlyValTyrMetSerGlu 164
DB 789 ATCCCTACGGACATCTACAAGGCTCCACATGTCATCTCAATGAGCTCAACTGGACAGAG 848
QY 165 AlaLeuAsnAlaValPheValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyr 184

DB 849 GCCTGGAGAAATGTGTTCTGTGAAACCGCAGACAAGACCCACACTGTGTGGCAGGTC 908
QY 185 PheGlySerAlaThrGlyPhePheArgIleTyrProGlyIleLysTyrThrProAspGlu 204
DB 909 TTCGGCAGCGCCACAGGAGTCACTCGCTACTACCCGGCCACCCCGTGGCGAGCCCCCAAG 968
QY 205 AsnGlyValIleThrPheAspCysArgAsnArgGlyTyrTyrIleGlnAlaAlaThrSer 224
DB 969 AAG---ATCGACCTGTACGATGCCGAGGAGACCTGGTATATATCCAGGGGGCTCGTCA 1025
QY 225 ProLysAspIleValIleLeuValAspValSerGlySerMetLysGlyLeuArgMetThr 244
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QY 245 IleAlaLysHisThrIleThrIleLeuAspThrLeuGlyGluAsnAspPheValAsn 264
DB 1086 CTGATGAAGACATCTGTCTGCGAGATGCTGGACCGCTGCTGATGATGACTATGTGAAT 1145
QY 265 IleAlaLysAsnAspTyrValHisTyrIleGluProCysPheLysGlyIleLeuVal 284
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QY 285 GlnAlaAspArgAsnArgGluHisPheLysLeuValGluGluLeuMetValLys 304
DB 1200 CAGGCCAATGTGCGCAACAAGAGGTGTTCAAGGAGCTGTGCGGCGCATGGTGGCCAAAG 1259
QY 305 GlyValGlyValValAspGlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGln 324
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QY 325 GluAlaLysGlnGlySerLeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaVal 344
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QY 345 GluAspTyrGluProValPheGluLysTyrAsnTyrProAspCysLysValArgValPhe 364
DB 1374 GACCGCGTCGAGGACGCTCTTTGAGAAGTACAATTGGCCAAACCGGCGCGCTGTTT 1433
QY 365 ThrTyrLeuIleGlyArgGluValSerPheAlaAspArgMetLysTyrIleAlaCysAsn 384
DB 1434 ACTTTCCTGGTGGGCGCATTAATACTATGAGTCACACCGCTGCGATGGATGGCTGTGCC 1493
QY 385 AsnLysGlyTyrTyrThrGlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGlu 404
DB 1494 AACAAAGGCTACTATTTGAGATCCCTTCATCGGAGCCATCCGTCATCAACACACAGGAA 1553
QY 405 TyrLeuHisValLeuSerArgProMetValIle-----AsnHisAspHisAspIleIle 422
DB 1554 TATCTAGATGTGTGGCGAGGCCCATGGTGTGGCAGGCAAGGAGCCCAAGCAGGTTTCAG 1613
QY 423 TrpThrGluAlaTyrMetAspSerLysLeuLeuSerSerGlnAlaGlnSerLeuThrLeu 442
DB 1614 TGGACCAACGTGTATGAGGAT-----GCACTGGGACTGGGGTTG 1652
QY 443 LeuThrThrValAlaMetProValPheSer-----LysLys 454
DB 1653 GTGGTAAACAGGAGCCCTCCCTGTTTTCACACTGACACAGGATGGCCCTGGGGAAGAAAG 1712
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DB 1713 AACCAAG-----CTGATCTGGGCGTGTATGGGCATTGACGGCTCTGAAT 1757
QY 475 GluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyrAlaPheLeuAsn 494
DB 1758 GACATCAAGAGGCTGACCCCAACTACAGCTTGGAGCCAAACGGCTATGTGTTTGGCAAT 1817
QY 495 ThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeu-----TyrArg 511
DB 1818 GACCTGACCGGCTACGTTGTGTGTCACCCCAATCTCAAGCCCGCAGCCACCACTTCCGG 1877
QY 512 GluGlyLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluValGlu 531
DB 1878 GAGCCTGTGACTCTG-----GACTTCCTGGATGGGAG 1910

Qy	532	TrpGluAspGln----	AlaGluSerLeuArgThrAlaMetIleAenArgGluThrGlyThr	550
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Qy	551	LeuSerMetAspValIlyValProMetAspIysGlyIysArgValLeuPheLeuPheLeuAsn	570	
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Qy	571	AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg	590	
Db	2031	AACTACACCTGGGTGGCTATTAAGGAGCACTAACTACAGCCTGGGCTGGTCTCCACCC	2090	
Qy	591	GlyHisGlyGluTyrIle-----	596	
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Qy	597	-----LeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeuLeuHisProAsp	614	
Db	2151	GAGTTCCTGCTCCCGCAGCGTTTGAGCTGTGAGGA---CACGTTTTCATTGTCTCCAGA	2207	
Qy	615	LeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspProAspHisArgLys	634	
Db	2208	-----GAGTACTGC---AAGGACCTGAATGCCTCAGACAACAAC	2243	
Qy	635	LeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspProAsp---LeuGlu	653	
Db	2244	ACCGAGTTCCTGAAACAACTTTATTGAGCTCATGGAGAAAGTGACTCCAGACTCCAAAGCAG	2303	
Qy	654	CysAspGluLeuLeuValArgGluValLeuPheAspAlaValValThrAlaProMet---	672	
Db	2304	TGCACAACACTTCCTCTGTCACAACCTGATCTTGACACGGGCATCAGCAGCAGCTGGTA	2363	
Qy	673	GluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisValValAsp	692	
Db	2364	GAGCGTGTGGAGGGACAGGATCTCAAC-----ACGTACAGCCTACTG	2408	
Qy	693	MetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGlySerGlu	712	
Db	2409	GCGGTGTTCCTGCCACAGACGGTGGCATCACCCGA-----	2444	
Qy	713	LysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThrLeuAsp	732	
Db	2445	-----GTCTTCCCAACNAGGCAGCTGAGGACTGGACAGAGAAC	2483	
Qy	733	ArgPheProLeu-----TrpTyrArgGlnAlaSerGluHisProAlaGlySerPhe	749	
Db	2484	CCTGAGCCCTTCAATGCGCAGCTTCTACCGCGCAGCCTGGATAAC-----CACGGTTAT	2537	
Qy	750	ValPheAsn-----LeuArgTrpAlaGluGlyPro---GluSer	761	
Db	2538	GTCTTCAAGCCCCCACACAGGATGCCCTGTTAAG-----CCGTGGAGCTG	2585	
Qy	762	AlaGlyGluProMetValValThrAlaSerThrAlaValAlaValThrValAspLysArg	781	
Db	2586	GAGNATGACACTGTGGGCATCTCCGTGACGACAGCTGTGTGAGCTCAGCCTAGCAGGCGC	2645	
Qy	782	ThrAlaIleAlaAlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLysPhe	801	
Db	2646	ACACTGAGGCCAGCAGTGGTGGGCGCTCAAGCTGGACCTAGAGGCTTGGGCTGAGAAGTTC	2705	
Qy	802	TrpAlaAlaThrArgGlnCysSerThrValAspGlyProTyrThrGlnSerCys-----	819	
Db	2706	AAGTGTGTGCCAGCAACCGTATCCCAAGACAGACGCT-----CAGAAGTCGGGCCCC	2759	
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Db	2760	AACAGCCACTGTGATGGACTCGAGGTTAAACNATGAGGACTTACTCTGTGTCTCTATT	2819	
Qy	830	AspAsnAsnGlyPheIleLeuIleSerLysArgSerArg-----GluThrGlyArg	846	
Db	2820	GATGATGGAGGATTTCTGGTGTCTGTTCAACCAACCATCAGTGGACCAAGTGGGCAGG	2879	

Qy	847	PhelGlyGluValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSer	866
Db	2880	TTCTTCAGTGGAGTGATGCAACACCTGATGCTGGCACTCTACAAATACTCTTCTTCAACACC	2939
Qy	867	GlnValThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisHisSerAla	886
Db	2940	CGCAAGGAGTCCTATGACTATATCAGGCAGCTGTGCCCTCAGCCCCCTGGCAACCTGGGT	2999
Qy	887	AlaGlnPro-----LeuValSerProIleSerAlaPheLeu	898
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Qy	899	---ThrAlaThrArgTrpLeuLeuGlnLeuValLeuPheLeuLeuGluTyrPheSerVal	917
Db	3060	ACCTCTGCTGCCCGCTGGTCCCTGTTCAGCAGCTTCTCTACGGCCCTC-----ATC	3110
Qy	918	TrpGlySerTrpTyrAspArgGly-----AlaGluAlaLysSerValPheHisHis	934
Db	3111	TACCACAGCTGGTTTCCAAGCAGACCCCGCGGAGCCGAGGGAGCCCGAGACGCGCGAG	3170
Qy	935	SerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGluTyrProValPhe	954
Db	3171	AGCAGCTGCGTCATGAACACG-----ACCCAGTAC-----	3200
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Db	3201	---TACTTCGGCTCGGTAAAGCGCTCTCTACACGCCATCATCGACTCGCGAAACTGCTCC	3257
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Qy	993	ProThrCysAspCysSerIlePheProProValLeuGlnGluAlaThrGluValLysTyr	1012
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Db	3378	GACGGCCCGGAGCAGTGTGAGCTAGTGCAGAGACCCGGATACCGAGAGCGCCGCACATC	3437
Qy	1033	CysHisAlaPheHis---ProGluValAlaArgValGluAlaAspArgGlyTrpAlaGlyPhe	1051
Db	3438	TGCTTCGACTACAAACGCGACAGAAAGATACCTCAGACTGTGGCCCGCGG---GCCTCCTTC	3494
Qy	1052	-----SerSerProAsnProLeuCysLeuGlyLeuCysPro	1063
Db	3495	CCGCCGTGCTGGGGGTCTGTGTCCTCCCTGCAACTGCTGTCTCTCTGCGCCTTGC	3554
Qy	1064	CysArgGlnGluHisIleGlyMet-----ProMetAsnThr	1075
Db	3555	CGGCCGAGCTCAAGTCTCTCGTCCACGCGCTCTGCGCGCTCTGTGAGCACCTTGC	3614
Qy	1076	ProValProVal	1079
Db	3615	CCACCTCCACTC	3626

RESULT 12
US-09-470-443-3
; Sequence 3, Application US/09470443
; Patent No. 6441156
; GENERAL INFORMATION:
; APPLICANT: Lerman, Michael I.
; APPLICANT: Minna, John D.
; APPLICANT: Latif, Farida
; APPLICANT: Wei, Ming-Hui
; APPLICANT: Sekido, Yoshitaka
; APPLICANT: Gao, Boning
; APPLICANT: Duh, Fuh-Wei
; TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof
; FILE REFERENCE: NIH-05043
; CURRENT APPLICATION NUMBER: US/09/470,443
; CURRENT FILING DATE: 1999-12-22
; EARLIER APPLICATION NUMBER: 60/114,359


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; EARLIER FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 5482
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; ORIGIN:
; NAME/KEY: CDS
; LOCATION: (181)..(3618)
US-09-470-443-3

Alignment Scores:
Pred. No.: 2,28e-124 Length: 5482
Score: 1187.50 Matches: 348
Percent Similarity: 47.59% Conservative: 206
Best Local Similarity: 29.90% Mismatches: 429
Query Match: 20.74% Indels: 181
DB: 3 Gaps: 44

US-09-833-222A-10 (1-1090) x US-09-470-443-3 (1-5482)

QY 16 TrpAlaAspThrPheGlyAspLeuTyrAsnThrValThrLysTyrSerGlySerLeu 35
DB 397 TGGGCCCGCGCTCGGAGCAGGAGGTCGACCGCGTGTATGCGGATTTTGGAGCGCTCCAG 456
QY 36 LeuLeuGlnLysTyrLysAspValGluSerSerLeuLysIleGluGluValAspGly 55
DB 457 CAGCTCCGTGAGATTACAGGACAAACCGGAACCTGTTGAGGTACAGGAGATGAGCCT 516
QY 56 LeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArgArgLysValGlu 75
DB 517 CAGAAGTTGGTGAGAAAGTGGCAGGAGCATTTGAGAGCCTTCTGGACAGGAAGTGCAG 576
QY 76 AlaValGlnAsnLeuValGluAlaGluGluAlaAspLeuAsnHisGluPheAsnGlu 95
DB 577 GCCCTGAAGAGACTGGCTGTGTCAGAGAACTTCAGAAAGCACACACCGCTGGCAGGAC 636
QY 96 SerLeuValPheAsp-----TyrTyrAsnSerValLeuIleAsnGluArgAspGlu 112
DB 637 AACATCAAGGAGGAGACATCGTGTACTATGACGCCAAGCTGACGCTGAGCTGGAGCAG 696
QY 113 ---LysGlyAsnPheValGluLeuGlyAla-----GluPheLeu 124
DB 697 CCTGAGAGTGAGGATGTGGAAGAGGGGTCTAAGCCAGCACCCCTAAGGCTGGACTTCATC 756
QY 125 LeuGluSerAsnAlaHisPheSerAsnLeuProValAsnThrSerIleSerSerValGln 144
DB 757 GAGGACCCCAAC-----TTCAAGAAC--AAGGTCAACTATTTCATACGCGGTGTACAG 807
QY 145 LeuProThrAsnValTyrAsnLysAspProAspIleLeuAsnGlyValTyrMetSerGlu 164
DB 808 ATCCCTACGGACATCTACAAAGGCTCCACTGTCTATCTCAATGAGCTCAACTGGACAGAG 867
QY 165 AlaLeuAsnAlaValPheValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyr 184
DB 868 GCCCTGGAGAAATGTTTCATGGAACCCGACAGACAGACCCACACTGCTGTGGCAGGTC 927
QY 185 PheGlySerAlaThrGlyPhePheArgIleTyrProGlyIleLysTrpThrProAspGlu 204
DB 928 TTCGGAGCGGCCACAGAGGTCACTGCTACTACCGGCCCAACCCCGTGGGAGCCCCCAAG 987
QY 205 AsnGlyValIleThrPheAspCysArgAsnAtqGlyTyrTyrIleGlnAlaThrSer 224
DB 988 AAG---ATGACCTGTACGATGTCCAGAGGAGACCTGTTATATCCAGGGGCTCGTCA 1044
QY 225 ProLysAspIleValIleLeuValAspValSerGlySerMetLysGlyLeuArgMetThr 244
DB 1045 CCCAAAGACATGTCATCGTGGATGTGAGTGGCAGTGTGAGCGGCTGACCCCTGAAG 1104
QY 245 IleAlaLysHisThrIleThrIleLeuAspThrLeuGlyGluAsnAspPheValAsn 264
DB 1105 CTGATGAAGACATCTGTCTGCGGAGATGCTGGACACGCTGCTGTGATGATGATGATGAT 1164

265 IleIleAlaTyrAsnAspTyrValHisTyrIleGluProCysPheLysGlyIleLeuVal 284
DB 1165 GTGGCCTCGTTCAACAGGAGGACAGCGCTGTGTCA---TGCTTCACACAC---CTGGTG 1218
QY 285 GlnAlaAspArgAspAsnArgGluHisPheLysLeuValGluLeuMetValLys 304
DB 1219 CAGGCCAATGTGCGCAACAAGAAGTGTTCAGGAAGCTGTGCAGGGCATGGTGGCCAAG 1278
QY 305 GlyValGlyValValAspGlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGln 324
DB 1279 GGCACCACAGGCTACAAAGCGCGCTTGTAGTATGCTTTGACCAGCTGCAGAACTCCAAC 1338
QY 325 GluAlaLysGlnGlySerLeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaVal 344
DB 1339 ATCACTCGGGCCCAAC-----TGCAACAAGATGATCATGATTTACGATGTTGGTGAG 1392
QY 345 GluAspTyrGluProValPheGluLysTyrAsnTrpProAspCysLysValArgValPhe 364
DB 1393 GACCGCGTCGAGGACGCTCTTTCAGAAAGTACAATTGSCCAACCGGACGTCGCGTGT 1452
QY 365 ThrTyrLeuIleGlyArgGluValSerPheAlaAspArgMetLysTrpIleAlaCysAsn 384
DB 1453 ACTTTCTCCGTGGGCGAGCATAACTATGACGTCACACCGCTGCAGTGGATGGCTGTGCC 1512
QY 385 AsnLysGlyTyrTyrThrGlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGlu 404
DB 1513 AACAAAGGCTACTATTTTGAGATCCCTTCATCGGAGCATCCGTCATCAACACACAGGAA 1572
QY 405 TyrLeuHisValLeuSerArgProMetValIle-----AsnHisAspIleIle 422
DB 1573 TATCTAGATGTGTGGGAGGCCATCGTGTCTGGCAGGAGGAGGAGGAGGAGGAGGAGGAG 1632
QY 423 TrpThrGluAlaTyrMetAspSerLysLeuLeuSerSerGlnAlaGlnSerLeuThrLeu 442
DB 1633 TGGACCAACGCTGTATGAGGAT-----GCATGGGACTGGGGTGTG 1671
QY 443 LeuThrThrValAlaMetProValPheSer-----LysLys 454
DB 1672 GTGGTAACAGGAGGACCTCTCTGTTTCAACCTGACACAGGATGGCCCTGGGGAAGAAG 1731
QY 455 AsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAspValAlaLeuArg 474
DB 1732 AACCAAG-----CTGATCTCGGCGTGTATGGCATTCACGCTGATGTTGCCATT 1776
QY 475 GluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyrAlaPheLeuAsn 494
DB 1777 GACATCAAGAGGCTGACCCCAACTACACGCTTGGAGCCACGCGCTATGTTTGCATT 1836
QY 495 ThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeu-----TyrArg 511
DB 1837 GACCTGACGGCTACGTGTGTGTCACCCCACTCAAGCCCGGAGGAGGAGGAGGAGGAGG 1896
QY 512 GluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluValGlu 531
DB 1897 GACGCTGTGACTCTG-----GACTTCCTGGATGGGAG 1929
QY 532 TrpGluAspGln---AlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr 550
DB 1930 CTAGAGGATGAGAACCAAGGAGAGATCCGTCGAGCATGATTGATGGCAACAGGGCCAC 1989
QY 551 LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn 570
DB 1990 AAGCAGATCAGAACGTTGTCAGTCCCTGGATGAGAGGTACATAGATGAGGTGACACGG 2049
QY 571 AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg 590
DB 2050 AACTACACCTGGGTGCTATTAAGGAGCACTAACTACAGCCTGGGGCTGTGCTCCACCC 2109
QY 591 GlyHisGlyTyrIle----- 596
DB 2110 TACAGACCTCTTACTCTCAAGCCAACTCTCAGTGACCAGATCCTCGAGGTCAAGTATTT 2169
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Qy	597	-----LeuLeuGlyAenThrSerValGluGluGlyLeuHisAspLeuLeuHisProAsp	614
Db	2170	GAGTTCTGCTCCCGCAGCAGCTTTGAGTGTGAAGG---CACGTTTTTCATTGTCTCCGAGA	2226
Qy	615	LeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspProAspHisArgLys	634
Db	2227	-----GAGTACTGC---AAGGACCTCGAATGCTCTCAGACAACAAC	2262
Qy	635	LeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspProAsp---LeuGlu	653
Db	2263	ACCGAGTTCCTGAAAACTTTATTGAGCTCATGAGAAAGTGACTCCAGACTCCAAGCAG	2322
Qy	654	CysAspGluGluLeuValArgGluValuPheAspAlaValValThrAlaProMet---	672
Db	2323	TGCAACAACATTCCTCTCTGCACAACCTGATCTTGGACACGGGCATCAGCAGCAGCTGGTA	2382
Qy	673	GluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisValValAsp	692
Db	2383	GAGCGTGTGTGAGGGACCGAGGATCTCAAC-----ACGTACAGCCTACTG	2427
Qy	693	MetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGlySerGlu	712
Db	2428	GCCGTGTTGCTGCCACAGACGAGCGGTGGCATCACCGA-----	2463
Qy	713	LysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThrLeuAsp	732
Db	2464	-----GTCTTCCCAACAAGGCAGCTGAGGACTGGACAGAGAAC	2502
Qy	733	ArgPheProLeu-----TrpTyrArgGlnAlaSerGluHisProAlaGlySerPhe	749
Db	2503	CCTGAGCGCCTTCAATGCCAGCTTCTACCGCGCAGCCTGGATAAC-----CACGGTTAT	2556
Qy	750	ValPheAsn-----LeuArgTrpAlaGluGlyPro---GluSer	761
Db	2557	GTCTTCAAGCCCCCACACCGAGGATGCCTGTTAAG-----CGCTGGAGCTG	2604
Qy	762	AlaGlyGluProMetValValThrAlaSerThrAlaValAlaValThrValAspLysArg	781
Db	2605	GAGAAATGACACTGTGGGCATCTCTCGTCAGCACAGCTGTGGAGCTTCAGCCTAGGCAGGCGC	2664
Qy	782	ThrAlaIleAlaAlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLysPhe	801
Db	2665	ACACTGAGCCAGCAGCTGGTGGCGCTCAAGCTGGACCTAGAGGCTTGGGCTGGAAGTTC	2724
Qy	802	TrpAlaAlaThrArgGlnCysSerThrValAspGlyProTyrThrGlnSerCys----	819
Db	2725	AAGGTGTAGCCAGCAACCGTACCACCAAGACCAGCCT-----CAGAAGTGGCGCCC	2778
Qy	820	-----GluAspSerAspLeuAspCysPheValIle	829
Db	2779	AACAGCCACTGTGAGATGGAGTGCAGGTTAAACAATGAGGACTTTACTCTGTGTCTCATTT	2838
Qy	830	AspAsnAsnGlyPheIleLeuIleSerLysArgSerArg-----GluThrGlyArg	846
Db	2839	GATGATGAGGATTCCTGGTGCTGTCAAAACAGAACCATCAGTGGGACCAAGGTGGGCGAGG	2898
Qy	847	PheLeuGlyGluValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSer	866
Db	2899	TTCTTCAGTGAGGTGGATGCCAACCTGATGCTGGCACTCTACATAACTCTCTCTACACC	2958
Qy	867	GlnValThrMetTyrAspTyrGlnAlaMetCysLysProSerHisHisSerAla	886
Db	2959	CGCAAGGAGTCCTATGACTATCAGGAGCCTGTGCCCTCAGCCCCCTGGCAACCTGGGT	3018
Qy	887	AlaGlnPro-----LeuValSerProIleSerAlaPheLeu-----	898
Db	3019	GCTGCACCCGGGTGTCTTTGTGTGCCACCGTTCAGATTTCTCTTAACCTGGCCTGGTGG	3078
Qy	899	--ThrAlaThrArgTrpLeuLeuGlnGluLeuValLeuPheLeuLeuGluTrpSerVal	917
Db	3079	ACCTCTGCTGCCGCTGTCTCTTCCACAGAGCTTCTCTACGGCTC-----ATC	3129
Qy	918	TrpGlySerTrpTyrAspArgGly-----AlaGluAlaLysSerValPheHisHis	934

[illegible]


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Qy 733 ArgPheProLeu-----TrpTyrArgGlnAlaSerGluHisProAlaGlySerPhe 749
Db 2503 CCTGAGCCCTTCAATGCCAGCTTCTACCGCGCAGCTGGATAAC-----CACGGTTAT 2556
Qy 750 ValPheAsn-----LeuArgTrpAlaGluGlyPro---GluSer 761
Db 2557 GTCTTCAAGCCCCACACACAGGATGCCCTGTTAAG-----CCGCTGAGAGCTG 2604
Qy 762 AlaGlyGluProMetValThrAlaSerThrAlaValAlaValThrValAspLysArg 781
Db 2605 GAGATGACACTGTGGCATCTCTCGTCAGACAGCTGTGGAGCTCAGCCTAGGAGCGGC 2664
Qy 782 ThrAlaIleAlaAlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLysPhe 801
Db 2665 AACTGAGGCGCAGTGGTGGCGTCAAGCTGAGCCTAGAGGCTTGGGCTGAGAGAGTTC 2724
Qy 802 TrpAlaAlaThrArgGlnCysSerThrValAspGlyProTyrThrGlnSerCys----- 819
Db 2725 AAGGTGCTAGCCAGCAACCGTACCACCAAGACAGCCT-----CAGAAGTGGCGCCC 2778
Qy 820 -----GluAspSerAspLeuAspCysPheValIle 829
Db 2779 AACAGCCACTGTGAGATGGAGTGCAGAGTTAACTAGGACTTACTGTGTCTCTCAT 2838
Qy 830 AspAsnAsnGlyPheIleLeuIleSerLysArgSerArg-----GluThrGlyArg 846
Db 2839 GATGATGAGGATTCCTGGTGTCTCAACAGAACCATCAGTGGGACAGGTGGGCGAG 2898
Qy 847 PheLeuGlyGluValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSer 866
Db 2899 TTCTTCACTGAGTGGATGCCAACCTGATGTGGCACTCTACAATAACTCTCTTACACC 2958
Qy 867 GlnValThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisSerAla 886
Db 2959 CGCAAGAGTCTTATGACTATCAGGACCTGTGCCCTCAGCCCTCGCAACCTGGGT 3018
Qy 887 AlaGlnPro-----LeuValSerProIleSerAlaPheLeu----- 898
Db 3019 GCTGCACCCCGGGGTGCTTTGTGCCACCGTGGCAGATTCTTAACCTGGCTGGTG 3078
Qy 899 ---ThraAlaThrArgTrpLeuLeuGlnGluValLeuPheLeuLeuTrpSerVal 917
Db 3079 ACCTCTGCTCGGCTGTGCTTCCAGCAGCTTCTTACGCGCTC-----ATC 3129
Qy 918 TrpGlySerTrpTyrAspArgGly-----AlaGluAlaLysSerValPheHisHis 934
Db 3130 TACCACAGCTGGTTCCAAAGCAGACCCCGCGAGCGCGAGGAGCCCGCAGCGCGAG 3189
Qy 935 SerHisLysHisLysGlnAspProLeuGlnProCysAspThrGluTyrProValPhe 954
Db 3190 AGCAGCTGCTCATGAACAG-----ACCCAGTAC----- 3219
Qy 955 ValTyrGlnProAlaIleArgGluAla---AsnGlyIleValGluCysGlyProCysGln 973
Db 3220 ---TACTTCGGCTCGGTAAACGGCTCTACAACGCCATCATCGACTCGGAAACTGCTCC 3276
Qy 974 LysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuValThrAsp--- 992
Db 3277 AGGCTGTTCACGCGCAGAGACTGACCAACCACTCTCTTTTGGTGGCGGAGAG 3336
Qy 993 ProThrCysAspCysSerIlePheProValLeuGlnGluAlaThrGluValLysTyr 1012
Db 3337 CCGCTGTGCAGCCNGTCCGAGGTGGCGGCTGTCGAGAGGAGAGCAGCCTGCCACGC 3396
Qy 1013 AsnAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgArgProAspSer 1032
Db 3397 GACGCCCGGAGCAGTGTGAGCTAGTCAGAGACCGCGATACCGAGAGGCCCGCACATC 3456
Qy 1033 CysHisAlaPheHis-----ProGluValArgValGluAlaAspArgGlyTrpAlaGlyPhe 1051
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Qy 1052 -----SerSerProAsnProLeuCysLeuGlyLeuCysPro 1063
Db 3514 CGCCCGTGGTGGCGCTCTGCTCTCCTGCAACTGCTGCTCTCTCTCTCTCTCTCTCT 3573
Qy 1064 CysArgGlnGluHisIleGlyMet-----ProMetAsnThr 1075
Db 3574 CGCCCGCAGCCTCAAGTCTCTGCTCCACGCTCTCTCGCGCTCTCTGAGCACCTCT 3633
Qy 1076 ProValProVal 1079
Db 3634 CCACCTCCACTC 3645

RESULT 14
US-09-397-550-3
; Sequence 3, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCE: 180
; CURRENT APPLICATION NUMBER: US/09/397,550
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3327
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-397-550-3

Alignment Scores:
Pred. No.: 7, 63e-124 Length: 3327
Score: 1179.50 Matches: 332
Percent Similarity: 48.33% Conservative: 202
Best Local Similarity: 30.05% Mismatches: 408
Query Match: 20.60% Indels: 163
DB: 4 Gaps: 40

US-09-833-222A-10 (1-1090) x US-09-397-550-3 (1-3327)
Qy 16 TrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLysTyrSerGlySerLeu 35
Db 217 TGGCCCGCGCTCTGGAGCAGGAGTCCGCGGTGATCGGATTTTGGAGGCGTCCAG 276
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Db 277 CAGCTCCGTGAGATTTTACAAGGACAACCGGAACCTGTTCGAGGTACAGGAGATGAGCCT 336
Qy 56 LeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArgAspLysValGlu 75
Db 337 CAGAGTTGTGTGAGAGAGTGGCGGGGACATTGAGAGCCTTCTGGACAGAGAGTGCAG 396
Qy 76 AlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsnHisGluPheAsnGlu 95
Db 397 GCCTTGAAGAGACTGGCTGATGCTGCAGAGAACTTCCAGAAAGCACACACCGCTGCAGGAC 456
Qy 96 SerLeuValPheAsp-----TyrTyrAsnSerValLeuIleAsnGluArgAspGlu 112
Db 457 AACATCAAGGAGGAGAACACATCGTGTACTATGACCCCAAGGCTGACGCTGAGCTGGAGCAG 516
Qy 113 ---LysGlyAsnPheValGluLeuGlyAla-----GluPheLeu 124
Db 517 CTGAGAGTGAAGATGTGAAAGGGGCTTAAGCCGACACCTTAAGGTGGACTTTCATC 576
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Db 577 GAGGACCCAAAC-----TTCAAGAAC---AAGGTCAACTATTTCATACGGCGGTGTACAG 627
Qy 145 LeuProThrAsnValTyrAsnLysAspProAspIleLeuAsnGlyValTyrMetSerGlu 164
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Db 688 GCCTTGAGAAATGTTTCATGGAAACCGGACAGAACAGCCACACTGCTGTGGCAGGTC 747
Qy 185 PheGlySerAlaThrGlyPhePheArgIleTyrProGlyIleYsTrpThrProAspGlu 204
Db 748 TTCGGACCGCCACAGAGTCACTCGCTACTACCCGGCCACCCGCTGGCGAGCCCCCAAG 807
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Db 808 AAG---ATCGACCTGTACGATGTCGGAAGAGACCCCTGGTATATTCAGAGGGGGCTCGTCA 864
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Db 865 CCCAAGACATGGTCATCATCGTGATGTGAGTGGCAGTGTGAGCGGCCTGACCCCTGAAG 924
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Qy 325 GluAlaLysGlnGlySerLeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaVal 344
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Qy 365 ThrTyrLeuIleGlyArgGluValSerPheAlaAspArgMetLysTrpIleAlaCysAsn 384
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Qy 385 AsnLysGlyTyrTyrThrGlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGlu 404
Db 1333 AACAAAGGCTACTATTTTGAGATCCCTTCCATCGAGCCATCCGCATCAACACACAGGAA 1392
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Qy 423 TrpThrGluAlaTyrMetAspSerLysLeuLeuSerSerGlnAlaGlnSerLeuThrLeu 442
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Qy 443 LeuThrThrValAlaMetProValPheSer-----LysLys 454
Db 1492 GTGTGAACAGGAGCCCTCCCTGTTTTCACACCTGCACAGGATGGCCCTGGGGAAGAAG 1551
Qy 455 AsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAspValAlaLeuArg 474
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Db 1597 GACATCAAGAGGCTGACCCCACTACACGCTTGGAGCCAAACGGCTATGTGTTGCCATT 1656
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Db 1717 GAGCCTGTGACTCTG-----GACTTCCTGGATGGGAG 1749
Qy 532 TrpGluAspGln---AlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr 550
Db 1750 CTAGAGATGAGAACAGGAGAGATCCGTCGGAGCATGATTGATGGCAACAAGGGCCAC 1809
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Qy 597 -----LeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeuLeuHisProAsp 614
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Qy 615 LeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspProAspHisArgLys 634
Db 2047 -----GAGTACTGC---AAGACCTGAATGCCTCAGACAACAAC 2082
Qy 635 LeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspProAsp---LeuGlu 653
Db 2083 ACCGAGTTCTCTGAAAACTTTATTGAGTCTATGGAGAAAGTGACTCCAGACTCCAAGCAG 2142
Qy 654 CysAspGluGluLeuValArgGluValLeuPheAspAlaValValThrAlaProMet--- 672
Db 2143 TGCACAACACTTCTCTGCACAACCTGATCTTTGGACACCGGCATCACGACGAGCTGGTA 2202
Qy 673 GluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisValValAsp 692
Db 2203 GAGCGTGTGGAGGACCAAGGATCTCAAC-----ACGTACAGCCTACTG 2247
Qy 693 MetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGlySerGlu 712
Db 2248 GCGGTGTTTCGCTGCCACAGACAGCGTGGCATCACCCGA----- 2283
Qy 713 LysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThrLeuAsp 732
Db 2284 -----GTCTTCCCAACAAGGCGAGCTGAGGACTGGACAGAGAAC 2322
Qy 733 ArgPheProLeu-----TrpTyrArgGlnAlaSerGluHisProAlaGlySerPhe 749
Db 2323 CCTGAGCCCTTCATGCGCAGCTTCTACCGCGAGCCTGGATAAC-----CACGGTTAT 2376
Qy 750 ValPheAsn-----LeuArgTrpAlaGluGlyPro---GluSer 761
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Qy 762 AlaGlyGluProMetValValThrAlaSerThrAlaValAlaValThrValAspLysArg 781
Db 2425 GAGAAATGACACTGTGGGCATCTCTCGTCACACAGCTGTGGAGCTCAGCTAGCGAGCGC 2484
Qy 782 ThrAlaIleAlaAlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLysPhe 801
Db 2485 ACACCTGAGCCAGCAGTGTGGCGCTCAAGCTGGACCTAGAGGCTGGGCTGAGAAGTTC 2544
Qy 802 TrpAlaIaThrArgGlnCysSerThrValAspGlyProTyrThrGlnSerCys----- 819
Db 2545 AAGGTGCTAGCCAGCAACCGTACCACCAAGACCAGCCT-----CAGAAGTGGCGCCC 2598
Qy 820 -----GluAspSerAspLeuAspCysPheValIle 829
Db 2599 AACAGCCACTGTGAGATGAGCTGCGAGGTTAAACAATGAGGACTTACTCTGTGTCTCAT 2658

Db 3157 CCGCTGTGACCCAGTCGAGGCTGGCCGCTGCTGCAGAAAGGAGACGCCACTGCCACGC 3216
Qy 1013 AsnAlaSerVallysCysAsp 1019
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Db 3217 GACGCCCGGAGCAGTGTGAG 3237

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Job time : 602 secs

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OM protein - nucleic search, using frame_plus_p2n model

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(without alignments)
5174.614 Million cell updates/sec

Title: US-09-833-222A-10

Perfect score: 5726

Sequence: 1 MAVALGTRRRDRVKLWADF.....MPMNTVPVLLGGNIRVYAL 1090

Scoring table:

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Ygapop 10.0	Ygapext 0.5	
Fgapop 6.0	Fgapext 7.0	
Delop 6.0	Delext 7.0	

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=EST -QPM=fastcap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPT=0 -LOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-OUTALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO MMAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:

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5:	gb_est5.*
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8:	gb_est8.*
9:	gb_est9.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2593.5	45.3	2730	9 AY404364	AY404364 Homo sapi
2	2591	45.2	2690	9 AY404366	AY404366 Mus muscu
3	2493.5	43.5	2730	9 AY404365	AY404365 Pan trogl
4	2241	39.1	2583	3 AK030723	AK030723 Mus muscu
5	1800.5	31.4	3230	3 AK044427	AK044427 Mus muscu
6	1356	23.7	916	4 BF158624	BF158624 603061574
7	1317.5	23.0	892	1 AL558158	AL558158 AL558158
8	1297	22.7	1446	3 CR603629	CR603629 full-leng
9	1266	22.1	747	6 CD743170	CD743170 UI-H-Ftl-

10	1246.5	21.8	853	4	BI908421	603067367
11	1228	21.4	765	7	CO424223	UI-M-HUO-
12	1208	21.1	940	5	BQ193363	AGENCOURT
13	1182.5	20.7	777	4	BI908463	603069223
14	1180	20.6	3527	3	AK044603	Mus muscu
15	1157.5	20.2	725	4	BG436760	602489181
16	1136	19.8	942	5	BU155034	AGENCOURT
17	1130	19.7	776	7	CNS39658	UI-M-HUO-
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22	1029	18.0	893	6	CD513443	AGENCOURT
23	985.5	17.2	3675	3	AK014825	Mus muscu
24	974	17.0	842	6	CD107126	AGENCOURT
25	958	16.7	688	4	BI871869	603396817
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27	931	16.3	794	7	CK130243	AGENCOURT
28	928.5	16.2	816	7	CK130243	AGENCOURT
29	927	16.2	779	7	CK130239	AGENCOURT
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32	901.5	15.7	2791	9	AY403434	Homo sapi
33	898.5	15.7	852	5	BX329163	BX329163
34	897.5	15.7	2750	9	AY403436	Mus muscu
35	894	15.6	713	7	CK130240	AGENCOURT
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38	854	14.9	498	5	BQ636196	hd05908.Y
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45	790.5	13.8	522	2	AW656606	108945 MA

ALIGNMENTS

RESULT 1	AY404364	2730 bp	DNA	linear	GSS 15-DEC-2003
LOCUS	AY404364	Homo sapiens CACNA2D3 gene, VIRTUAL TRANSCRIPT, partial sequence,			
DEFINITION	AY404364	genomic survey sequence.			
ACCESSION	AY404364.1	GI:39760341			
VERSION	AY404364.1	GI:39760341			
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 2730)				
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarial, A., Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Infering nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 2730)				
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarial, A., Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.				
FEATURES	Location/Qualifiers				
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ORIGIN		/locus_tag="HCM1866"			
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Best Local Similarity:	53.69%	Mismatches:	248		
Query Match:	45.29%	Indels:	18		
DB:	9	Gaps:	7		
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Qy	154	ProAspIleLeuAenGlyValTyrMetSerGluAlaLeuAenAlaValPheValGluAen	173	LysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProVal	450
Db	1	CCTGCAATTGTCANTGGGGTTATTGGTCTGAATCTCTAAACAAAGTTTTTGTAGATAAC	60	NN	900
Qy	174	PheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPheArg	193	PheSerLysLysAenGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp	470
Db	61	TTTGACCGTGACCCATCTCTCATATGGCAGTACTTTTGGAAAGTGCAAAGGGCTTTTATAGG	120	NN	960
Qy	194	IleTyrProGlyIleLysTrpThrProAspGluAenGlyValIleThrPheAspCysArg	213	ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyr	490
Db	121	CAGTATCCGGGGATTAAATGGGAACCCAGATGGAATGGAGTCAATGCTTCGACTCGAGG	180	GTCCCAAGTGAAGAACTTCTGAAGACCATCCCAAAATACAAGTTAGGATTCACGGTTAT	1020
Qy	214	AenArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIleLeuValAsp	233	AlaPheLeuAenThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr	510
Db	181	AACCGAAATAGGTACATCCAGGAGCAACTTCTCCGAAAGACGTGTCAATTTAGTTGAC	240	GCCTTTGCAATACAAATAATGGATATATCTCTGAGCATCCGAACTCAGGCTGCTGTAC	1080
Qy	234	ValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThrIle	253	ArgGluGlyLysLysProLysProAsnTyrAsnSerValAspLeuSerGluVal	530
Db	241	GTCAAGTGGCAGCATGAAGGACTCCGTCTGACTATCGCAAGCAACAGTCTCATCAATT	300	GAAGAAGGAAAGAG--CGAAGGAACCTTAATACTAGTAGCCTTCTGAGGTG	1137
Qy	254	LeuAspThrLeuGlyGluAenAspPheValAenIleIleAlaTyrAenAspTyrValHis	273	GluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAenArgGluThrGlyThr	550
Db	301	TTGGATACACTTGGGATGATGACTTCTTCAACATAATTGCTTTATATAGGAGCTTCAC	360	GAGTGGAAAGACCGAGATGACGTGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	1197
Qy	274	TyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAenArgGluHis	293	LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn	570
Db	361	TATGTGAACCTTGCCCTGAATGGAACTTTGGTCCAGCCGACAGCAACAAAGAGCAC	420	NNNNCCATGGAGGTGAAGAAGACAGTGGACAAAGGGAACCGGTTTGGTGATGACAAAT	1257
Qy	294	PheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAspGlnAlaLeu	313	AspTyrPhePheThrAspIleSerAspThrPropheSerLeuGlyAlaValLeuSerArg	590
Db	421	TTCAGGAGCATCTGGACAAACTTTTCGCCAAAGGAATTGGAATGTTGGATATAGCTCTG	480	GACTACTATTATACAGACATCAAGGTACTCTCTTCAGTTTAGTGTGGCGCTTTCCAGA	1317
Qy	314	ArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySerLeuCysAen	333	GlyHisGlyGluTyrIleLeuLeuGlyAenThrSerValGluGluGlyLeuHisAspLeu	610
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Db	601	NN	660	GAGCAGCCCATCTGTCTCAGTTAGAGCGATTAGCTTACCTTAAAGCAAGAACCT	1497
Qy	374	PheAlaAspArgMetLysTrpIleAlaCysAenLysGlyTyrTyrThrGlnIleSer	393	AspLeuGluCysAspGluLeuValArgGluValLeuPheAspAlaValValThrAla	670
Db	661	TTTGACAGCAATCTAAAGTGATGGGCTGTGCCAACAAAGGATTTTATACCAAGATCTCC	720	CTGCTCCAGTGTGATAAAGAAATTGATCCAAAGAGTCTTTTTCACGCGGTGTGAGTGCC	1557
Qy	394	ThrLeuAlaAspThrGlnGluAenValMetGluTyrLeuHisValLeuSerArgProMet	413	ProMetGluAlaTyrTrpThrAlaLeuAlaLeuAenMetSerGluGluSerGluHisVal	690
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Qy	414	ValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSer	430	ValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGly	710
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Qy 791 GlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThr 810
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Qy 811 ValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAsp 830
Db 1972 CTGGATGCCAATCTCCATCAGCTGTGATGATGAGACTGTGAATGTGACTCATAGAC 2031

Qy 831 AsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGlu 850
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Qy 851 ValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMet 870
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Qy 871 TyrAspTyrGlnAlaMetCysLeuProSerSerHisHisSerAlaAlaGlnProLeu 890
Db 2152 TATGACTACCCAGCCATGTGTAGAGCCCAACAGAAAGACGCGATGGCGCCATGGGCTC 2211

Qy 891 ValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluValLeu 910
Db 2212 CTGGATCCTTATATGCTTCTCTCGAGTAAATGGATCATGACAGAACTTGTCTTG 2271

Qy 911 PheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSer 930
Db 2272 TTCCTGTGGAAATTTAACTCTGCG---AGTTGGTGGCACTCCGATATACAGCTTAAAGCC 2328

Qy 931 ValPheHisSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGlu 950
Db 2329 -----CAGAAATTTGAAACAGACCCTGGAGCCTTGTGATCTGAA 2367

Qy 951 TyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGly 970
Db 2368 TATCCAGCATTCGCTCTGAGCGGCACCATCAAGAGACTACAGGGAATATGCTTGTGAA 2427

Qy 971 ProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuVal 990
Db 2428 GACTGCTCCAAGTCTTGTTCATCCAGCAAAATCCCAAGCAGCAACCTGTTTCATGGTGTG 2487

Qy 991 ThrAspProThrCysAspCysSerIlePheProValLeuGlnGluAlaThrGluVal 1010
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Qy 1011 ---LysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgArgArg 1029
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Qy 1050 GlyPheSerSerProAsnPro 1056
Db 2661 TGCCCGCAGTCTCCAAGCCCA 2681

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RESULT 2
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 LOCUS Mus musculus CACNA2D3 gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.

ACCESSION
 AV404366
 VERSION AV404366.1 GI:39760343
 KEYWORDS GSS.

SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 1 (bases 1 to 2690)
 Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.

TITLE
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE
 2 (bases 1 to 2690)
 Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
 FEATURES
 Location/Qualifiers
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 Alignment Scores:
 Pred. No.: 9,74e-270 Length: 2690
 Score: 2591.00 Matches: 490
 Percent Similarity: 70.49% Conservative: 155
 Best Local Similarity: 53.55% Mismatches: 239
 Query Match: 45.25% Indels: 32
 DB: 9 Gaps: 8

US-09-833-222A-10 (1-1090) x AY404366 (1-2690)
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 Qy 194 IleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPheAspCysArg 213
 Db 121 CAGTACCAGGAGTAAATGGGAACCAAGATGAGAATGGAGTCATTTGCTGACGAG 180
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 Qy 274 TyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsnArgGluHis 293
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 Db 541 NNN 600

Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 Science 302 (5652), 1960-1963 (2003)
 14671302

2 (bases 1 to 2690)
 Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.

Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment.

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 /locus_tag="HCM1866"

gene
 ORIGIN
 Alignment Scores:
 Pred. No.: 9,74e-270 Length: 2690
 Score: 2591.00 Matches: 490
 Percent Similarity: 70.49% Conservative: 155
 Best Local Similarity: 53.55% Mismatches: 239
 Query Match: 45.25% Indels: 32
 DB: 9 Gaps: 8


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AY404365      AY404365      2730 bp      DNA      linear      GSS 15-DEC-2003
LOCUS         Pan troglodytes CACNA2D3 gene, VIRTUAL TRANSCRIPT, partial
DEFINITION    sequence, genomic survey sequence.
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VERSION       AY404365.1 GI:39760342
KEYWORDS      GSS.
SOURCE        Pan troglodytes (chimpanzee)
ORGANISM      Pan troglodytes
REFERENCE     1 (bases 1 to 2730)
AUTHORS       Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,
              Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
              Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
              Adams,M.D. and Cargill,M.
TITLE         Inferring nonneutral evolution from human-chimp-mouse orthologous
              gene trios
JOURNAL       Science 302 (5652), 1960-1963 (2003)
PUBMED       14671302
REFERENCE     2 (bases 1 to 2730)
AUTHORS       Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,
              Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
              Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
              Adams,M.D. and Cargill,M.
TITLE         Direct Submission
JOURNAL       Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
              Rockville, MD 20850, USA
COMMENT       This sequence was made by sequencing genomic exons and ordering
              them based on alignment.
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Alignment Scores:
Pred. No.:      4.1e-259      Length:      2730
Score:          2493.50      Matches:     473
Percent Similarity: 68.25%      Conservative: 146
Best Local Similarity: 52.15%      Mismatches:  271
Query Match:    43.55%      Indels:      18
DB:              9           Gaps:         7

US-09-833-222A-10 (1-1090) x AY404365 (1-2730)
Qy 154 ProAspIleLeuAenGlyValTyrMetSerGluAlaLeuAenAlaValPheValGluAen 173
Db 1 CCTGCAATTGCAATGGGGTTTATTGGTCTGAATCTCTAAACAAAGTTTTTGTAGATAAC 60
Qy 174 PheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhePheArg 193
Db 61 TTTGACCGTGACCCATCTCTCATATGGCAGTACTTTTGGAGTGCAGGCGGCTTTTAGG 120
Qy 194 IleTyrProGlyIleLeuThrProAspGluAenGlyValIleThrPheAspCysArg 213
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clone:A930012E17 product:hypothetical von Willebrand factor type A domain containing protein, full insert sequence.

ACCESSION AK044427

VERSION 1 GI:26090352

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Method. Enzymol. 303, 19-44 (1999)

99279253

PUBMED 10349636

REFERENCE

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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

20499374

PUBMED 11042159

REFERENCE

3

Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,

Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,

Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,

Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,

Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,

Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,

Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

20530913

PUBMED 11076861

REFERENCE

4

The RIKEN Genome Exploration Research Group Phase II Team and the

FANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

REFERENCE

5

The FANTOM Consortium and the RIKEN Genome Exploration Research

Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 3230)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,

Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,

Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,

Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,

Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,

Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,

Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,

Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,

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Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,

Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of

Physical and Chemical Research (RIKEN), Laboratory for Genome

Exploration Research Group, RIKEN Genomic Sciences Center (GSC),

RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,

Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,

URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,

Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.

Retina RNA was provided by Dr. Stefano Gustincich (Department of Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA 02115, USA) whose assistance is gratefully acknowledged. Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/

FEATURES

source

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1. 3230
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ORIGIN

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Best Local Similarity: 41.18% Mismatches: 21
Query Match: 31.44% Indels: 523
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US-09-833-222A-10 (1-1090) x AK044427 (1-3230)
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1 (bases 1 to 916)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: rsb@nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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US-09-833-222A-10 (1-1090) x BI518624 (1-916)

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 892)
Li.W.B., Gruber,C., Jesse,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequençage

```

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 6520.r.
 and it belongs to a clone representative of this cluster. For more
 information about this cluster and the virtual cDNA, see
 http://www.genoscope.cns.fr/cdna?c=CS0DJ001BG06QPI&c=6520.r.

FEATURES

source
 Location/Qualifiers
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 10-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and EcoR V into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
 Pred. No.: 6, 21e-132 Length: 892
 Score: 1317.50 Matches: 252
 Percent Similarity: 92.39% Conservative: 3
 Best Local Similarity: 91.30% Mismatches: 18
 Query Match: 23.01% Indels: 3
 DB: 1 Gaps: 2
 US-09-833-222A-10 (1-1090) x AL558158 (1-892)

Qy 789 GlyValGlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaLaThrArgGlnCys 808
 Db 3 GCGCTCCAAATGAAGTGGATTCCTCCAGCGCAATTCCTGGCGGCAACGCGCAGTGC 62
 Qy 809 SerThrValAspGlyProTyThrGlnSerCysGluAspSerAspLeuAspCysPheVal 828
 Db 63 AGCACTGTGGATGGCGGTGTCACACAGACAGTGCAGACAGTGTGCTGGACTGCTCGTC 122
 Qy 829 IleAspAenAnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyValArgPheLeu 848
 Db 123 ATCAGACAAACAGGGTTCATCTGATCTCCAGAGGTCCCGAGAGACGGAGAGATTCTG 182
 Qy 849 GlyGluValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnVal 868
 Db 183 GGGGAGGTGGATGGTGTCTCTGACCCAGCTGCTCAGCATGGGGTGTTCAGCAAGTG 242
 Qy 869 ThrMetTyraAspTyraGlnAlaMetCysLysProSerSerHisHisSerAlaAlaGln 888
 Db 243 ACTATGATGACTATCAGGCCATGTGCAAAACCTCGAGTACACACAGTGCAGGCCAG 302
 Qy 889 ProLeuValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeu 908
 Db 303 CCCCTG-----CCAAATTCGCTCTTTGACGGCGCAGGTGGCTGCTGCAGAGACTG 356
 Qy 909 ValLeuPheLeuLeuGluTrpSerValTrpGlySerTrpTyraAspArgGlyAlaGluAla 928
 Db 357 GTGCTGTTCTCTGCTGGAGTGGAGTGTCTGGGGCTCTCTGGTACGACAGAGGGCGCGAGGCC 416
 Qy 929 LysSerValPheHisHisSerHisLysLysLysGlnAspProLeuGlnProCysAsp 948
 Db 417 AAAAGTGTCTTCCATCTCCACAAACACAAAGAGCAGGACCCGCTGCAGCCCTCGCAC 476
 Qy 949 ThrGluTyraProValPheValTyraGlnProAlaIleArgGluAlaAenGlyIleValGlu 968
 Db 477 ACGAGTACCCCGTGTCTGTGTACNACCCGCCATTCGGGAGGCCAAGCGGATCTGTGAG 536

Qy 969 CysGlyProCysGlnLysValPheValValGlnGlnIleProAenSerAenLeuLeuLeu 988
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 Qy 989 LeuValThrAspProThrCysAspCysSerIlePheProProValLeuGlnGluAlaThr 1008
 Db 597 CTGTGTACAGACCCCTCTGTGACTGTGACATCTTCCACCATGCTGCAGAGCGGAC 656
 Qy 1009 GluValLysTyraAenAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgArg 1028
 Db 657 GAAGTCAATATATATGCTCTGTCAATGTGACCGATGCGTCCCAAGAACTCCGCGG 716
 Qy 1029 ArgProAspSerCysHisAlaPheHisProGluValArgValGluAlaAspArgGlyTrp 1048
 Db 717 CGAMCAGACTCTCCACCGCTTCCATCCAGAGAGAAATGCCAG---GACTGCGGCGC 773
 Qy 1049 AlaGlyPheSerProAenProLeuCysLeuGlyLeuCysProCys 1064
 Db 774 SCTCGGACACCTCAGCTCGCGCCCTACTCCYGTGCTGTGTGT 821
 RESULT 8
 CR603629
 LOCUS
 DEFINITION
 full-length cDNA clone CS0DJ001YM12 of T cells (Jurkat cell line)
 Cot 10-normalized of Homo sapiens (human).
 CR603629
 VERSION
 CR603629.1 GI:50484436
 KEYWORDS
 HOMO; CNSLT; cDNA.
 SOURCE
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 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 1446)
 Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished
 JOURNAL
 CONTACT : feng liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue
 REFERENCE
 2 (bases 1 to 1446)
 Genoscope.
 AUTHORS
 Direct Submission
 TITLE
 Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
 JOURNAL
 COMMENT
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 FEATURES
 Location/Qualifiers
 1..1446
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DJ001YM12"
 /tissue_type="T cells (Jurkat cell line) Cot
 10-normalized"
 /plasmid="pCMVSPORT_6"
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 Score: 1297.00 Matches: 255
 Percent Similarity: 89.66% Conservative: 5
 Best Local Similarity: 87.93% Mismatches: 26
 Query Match: 22.65% Indels: 6
 DB: 3 Gaps: 2
 US-09-833-222A-10 (1-1090) x CR603629 (1-1446)
 Qy 789 GlyValGlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaLaThrArgGlnCys 808

Db 3 GGCCTCCAAATGAAGCTGAATTCCTCAGCGCAAAATTCGGCGCGCAACGCGCAGTCG 62

Qy SerThrValAspGlyProTyThrGlnSerCysGluAspSerAspLeuAspCysPheVal 828

Db 63 AGCACTGTGATGGCGCTGTCACACAGAGCTGCCAGGACAGTGTCTGGATCTGCTTCGTC 122

Qy IleAspAenAanGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeu 848

Db 123 ATCGACAAACAGGGTTCTATCTCATCTCCAAAGAGTCCCGAGAGACGGGAAGATTCTTG 182

Qy GlyGluValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnVal 868

Db 183 GGGAGGTGGATGCTGCTCTCAGCCAGCTGCTGAGATGGGGGTGTTTCAGCAAGTG 242

Qy ThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisHisSerAlaAaGln 888

Db 243 ACTATGATGACTATCAGCCATGTGCAAAACCTTCGAGTCACCAACAGTGCAGGCCAG 302

Qy ProLeuValSerProIleSerAlaPheLeuThrAlaThrArgTyrLeuLeuGlnGluLeu 908

Db 303 CCCCTG-----CCAATTTCTGCCTCTTGACGCGCAGCAGGTGCTGCTGCAGGAGCTG 356

Qy ValLeuPheLeuLeuGluTyrSerValTyrGlySerTyrTyrAspArgGlyAlaGluAla 928

Db 357 GTGCTGTCTCTGCTGGAGTGGAGTGTCTGGGGTCTCTGTGTACGACAGAGGGCGCGAGCC 416

Qy LysSerValPheHisHisSerHisLysHisLysLysGlnAspProLeuGlnProCysAsp 948

Db 417 AANAAGTGTCTTCATCTACTCCCAACACAAAGAGCAGGACCCGCTGCAGCCCTGGAC 476

Qy ThrGluTyrProValPheValTyrGlnProAlaIleArgGluAlaAanGlyIleValGlu 968

Db 477 ACGAGTACCCCGTGTGTGTACACGCGGCCCATCGGAGGCCAACGGGATCGTGAG 536

Qy CysGlyProCysGlnLysValPheValValGlnGlnIleProAenSerAenLeuLeu 988

Db 537 TGGGGGCCCTGCCAAGAGGTATTGTGTGTGTCAGCAGATTCCTCAACAGTAACCTCTCTCTC 596

Qy LeuValThrAspProThrCysAspCysSerIlePheProValLeuGlnGluAlaThr 1008

Db 597 CTGGTGACAGACCCACCTGTGACTGCAGATCTTCCACAGTGTCTGCAGAGGCGGACA 656

Qy Glu-----ValLysTyrAenAlaSerValLysCysAspArgMetArgSerGlnLysLeu 1026

Db 657 GAATGGCTCTGCA-CATAATGCTCTGTCAATGTGACCGGATGGCTCCAGAGCTC 715

Qy ArgArgArgProAspSerCysHisAlaPheHisProGluValArgValGluAlaAspArg 1046

Db 716 CGCGGGCGACAGACTCTGCCACGCTTCCATCCAGAGAGGAATGCCAGGACTGCGGC 775

Qy GlyTyrAlaGlyPheSerSerProAsnProLeuCysLeuGlyLeuCysProCysArgGln 1066

Db 776 GGGCGCTCGACACCTCAGCTCGCGCCCTACTCTCTGCT-GCCTGTGTGCTGCTGGG 834

Qy GluHisIleGlyMetProMetAenThrPro 1076

Db 835 GCTACTGCCCAACTCTCGGTGTCACACCA 864

RESULT 9

CD743170/c

LOCUS

DEFINITION

UI-H-FTI-bkc-o-08-0-UI.s1 NCI CGAP_FTI Homo sapiens cDNA clone

UI-H-FTI-bkc-o-08-0-UI 3', mRNA sequence.

CD743170

CD743170.1 GI:32294020

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 747)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL
COMMENT

Tumor Gene Index
Unpublished (1997)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>
The following repetitive elements were found in this cDNA
sequence: 183-231 ->HERV#LIR/Retroviral
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

Location/Qualifiers

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1..747
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="UI-H-FTI-bkc-o-08-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FTI"
/notes="Organ: Lung; Vector: p77T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI_CGAP_FTI is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Staph aureus moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p77T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FTI
TAG_SEQ=GGCATGCCG"

ORIGIN

Alignment Scores:

Pred. No.:	1,85e-126	Length:	747
Score:	1266.00	Matches:	231
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	22.11%	Indels:	0
DB:	6	Gaps:	0

US-09-833-222A-10 (1-1090) x CD743170 (1-747)

Qy 860 LeuSerMetGlyValPheSerGlnValThrMetTyrAspTyrGlnAlaMetCysLysPro 879
 Db 747 CTCAGCATGGGGGTTCAGCAAGTACTATGATGATATCATAGGCCATGTGCAAAACCC 688
 Qy 880 SerSerHisHisSerAlaGlnProLeuValSerProIleSerAlaPheLeuThr 899
 Db 687 TCGAGTCACACACACAGTGCAGCCCGCTGTGTGAGCCCAATTTCTGCCCTTCTTGACG 628
 Qy 900 AlaThrArgTrrpLeuLeuGlnGluLeuValLeuPheLeuLeuGluTrrpSerValTrpGly 919
 Db 627 CGCACCAGTGGCTGCTCAGGAGCTGGTGTCTCTGTCTGAGTGGAGTGTCTGGGGC 568
 Qy 920 SerTrrpTyrAspArgGlyAlaGluAlaLysSerValPheHisHisSerHisLysHisLys 939
 Db 567 TCCTGGTACGACAGAGGGCGGAGCCCAAAAGTGTCTTCATCATCTCCCAACAAACAAG 508
 Qy 940 LysGlnAepProLeuGlnProCysAepThrGluTrrpProValPheValTyrGlnProAla 959
 Db 507 AAGCAGGACCGCTGCAGCCCTGGACACGAGGTACCCCGTGTCTGTACCAACCCGGCC 448
 Qy 960 IleArgGluAlaAenGlyIleValGluCysGlyProCysGlnLysValPheValValGln 979
 Db 447 ATCCGGGAGGCCAACGGGATCGTGGAGTGGCGGCCCTGCCAGAGGTATTTGTGGTGCAG 388
 Qy 980 GlnIleProAenSerAenLeuLeuLeuValThrAspProThrCysAspCysSerIle 999
 Db 387 CAGATTCCCAACAGTAACCTCTCTCTCTGTGTGACAGACCCACCTGTGTACTGCAGCATC 328
 Qy 1000 PheProProValLeuGlnGluAlaThrGluValLysTyrAenAlaSerValLysCysAep 1019
 Db 327 TTCCACCAAGTCTGCAGAGCGCAGAGTCAATATATATGCTCTGTCAAAATGTGAC 268
 Qy 1020 ArgMetArgSerGlnLysLeuArgArgProAspSerCysHisAlaPheHisProGlu 1039
 Db 267 CGGATCGCTCCCAAGAGCTCCGCGCGGACACAGACTCTGTGCCACGCTTCCATCCAGAG 208
 Qy 1040 ValArgValGluAlaAepArgGlyTrrpAlaGlyPheSerSerProAenProLeuCysLeu 1059
 Db 207 GTGGGGTGTGAGGCGGATCGAGGGTGGGCTGGATTTTCATCCCAAAACCCCTCTGTGCTG 148
 Qy 1060 GlyLeuCysProCysArgGlnGluHisIleGlyMetProMetAenThrProValProVal 1079
 Db 147 GGTCTGTGCCCTCGACACAGAGCATATAGGATGCCAATGAACACACCTGTGCCCTGTG 88
 Qy 1080 LeuLeuGlyGlyAenIleArgValTyrAlaLeu 1090
 Db 87 CTTCTCGGGGAACATTCGGGTTTATGCCCTG 55

RESULT 10
 B1908421
 LOCUS 603067367F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5216273 5',
 DEFINITION mRNA sequence.
 ACCESSION B1908421
 VERSION B1908421.1 GI:16171373
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 853)
 NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: csapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

Plate: LLAM1543 row: f column: 18
 High quality sequence stop: 841.
 Location/Qualifiers
 source 1..853

/organism="Homo sapiens"
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 /clone="IMAGE:5216273"
 /tissue_type="leukocyte"
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 /clone_lib="NIH_MGC_118"
 /notes="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV
 (destroyed); RNA source leukocytes from anonymous pool of
 non-activated adult donors. Library is oligo-dT primed
 and directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.7 kb, insert size range
 1.2-3.3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 027. Note:
 this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
 Pred. No.: 3,08e-124 Length: 853
 Score: 1246.50 Matches: 247
 Percent Similarity: 87.32% Conservative: 1
 Best Local Similarity: 86.97% Mismatches: 13
 Query Match: 21.77% Indels: 23
 DB: 4 Gaps: 3

US-09-833-222A-10 (1-1090) x B1908421 (1-853)

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 Db 34 GCCCGGGCGTCCAAATGAAGCTGGAAATTCCTCCAGCGCAAAATTCCTGGCGGCAACGCGG 93
 Qy 807 GlnCysSerThrValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCys 826
 Db 94 CAG-----GATCTGGACTGC 108
 Qy 827 PheValIleAspAenGlyPheIleLeuIleSerLysArgSerArgGluThrGlyValArg 846
 Db 109 TTCTCATCGACAAACACCGGGTTCATTCGATCTCCAAAGAGGTCCCGAGAGACGGGAAGA 168
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 Db 169 TTCTCGGGAGGTGGATGGTGTCTGTGACCCAGCTGTCTAGCATGGGGTGTTCAGC 228
 Qy 867 GlnValThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisSerAla 886
 Db 229 CAAGTGACTATGTATGACTATCATAGGCCATGTGCAAAACCCCTCGAGTCAACACACAGTGCA 288
 Qy 887 AlaGlnProLeuValSerProIleSerAlaPheLeuThrAlaThrArgTrrpLeuGln 906
 Db 289 GCCCAGCCCTGTGTGACGCCCAATTTCTGCCCTCTTTCAGCGCAACAGGTGGTGTCTGCAG 348
 Qy 907 GluLeuValLeuPheLeuLeuGluTrrpSerValTrrpGlySerTrrpTyrAspArgGlyVal 926
 Db 349 GAGCTGGTCTGTCTCTGTGGAGTGGAGTGTCTGGGGCTCTCTGTGTACGACAGAGGGGCC 408
 Qy 927 GluAla-LysSerValPheHisSerHisLysHisLysLysGlnAepProLeuGlnPr 946
 Db 409 GAGGCCAAAAGTGTCTTCATCACTCCCAACAAACAAGAGCAGGACCCGCTGCAGCC 468
 Qy 946 OCysAspThrGluTrrpProValPheValTyrGlnProAlaIleArgGluAlaAenGlyIle 966
 Db 469 CTCGACAGCGAGTATACCCGTGTGTGTACAGCGCGCCATCCGGAGGCCAACCGGAT 528
 Qy 966 eValGluCysGlyProCysGlnLysValPheValValGlnGlnIleProAenSerAenLe 986
 Db 529 CGTGGAGTGGGGCCCTGCGCAGAAAGTATTTGTGTGTGACAGCATTTCCCAACAGTAACCT 588
 Qy 986 uLeuLeuValThrAspProThrCysAspCysSerIlePheProValLeuGlnG1 1006

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Db      CCTCCTCCTGTGTGACAGACCCACCTGTGTGCTGAGCATCTTCCACCAAGTGTGTGCAGGA 648
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Db      GGCACAGAAAGTCAAAATATATGCTCTGTCAAAATGTGACCGGATGGCTCCCAAGAAGC 708
Qy      euArgArgArgProAspSerCysHisAlaPheHisProGluValArgValGluAlaAspA 1046
Db      TCCGCGCGGACCAAGACTCTCGCCACCGCTTCCATCCAGAGGAGATGCCAG---GACT 765
Qy      rGGLyTTPAlaGlyPheSerSerProAsnProLeu-----CysLeuGlyL 1061
Db      GCGCGCGCGCTGGACACCTCAGCTTCGCGCCCTATCTCTGCTGCTGTGTGCTGCTGGGC 825
Qy      euCysPro 1063
Db      TACTGCCC 833

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RESULT 11
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DEFINITION UI-M-HU0-crd-n-17-0-UI.r1 NIH BMAP_HU0 Mus musculus cDNA clone
IMAGE:30666472 5', mRNA sequence.
CO424223
CO424223.1 GI:49670350
EST.
Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 765)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pYX-5.
Location/Qualifiers
1. 765
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30666472"
/tissue_type="whole eye"
/dev_stage="newborn( 1, 5, 15 days )"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_HU0"
/notes="Organ: Eye; Vector: pYX-Asc; Site:1: EcoR I;
Site:2: Not I; The library was constructed according
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AATAATTACG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."

```

FEATURES

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source
1. 765
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30666472"
/tissue_type="whole eye"
/dev_stage="newborn( 1, 5, 15 days )"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_HU0"
/notes="Organ: Eye; Vector: pYX-Asc; Site:1: EcoR I;
Site:2: Not I; The library was constructed according
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dt
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AATAATTACG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."

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ORIGIN

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Alignment Scores:
Pred. No.: 2,64e-122 Length: 765
Score: 1228.00 Matches: 233
Percent Similarity: 95.29% Conservative: 10
Best Local Similarity: 91.37% Mismatches: 12
Query Match: 21.45% Indels: 0
DB: 7 Gaps: 0

US-09-833-222A-10 (3-1090) x CO424223 (1-765)
Qy 395 LeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSerArgProMetVal 414
Db 1 CTGGCGGATGCGCAGGAGAGCGGTAGTACCTGATGTGCTTAGCCGCCCATGGTC 60
Qy 415 IleAsnHisAspHisAspIleIleThrGluAlaTyrMetAspSerLysLeuLeuSer 434
Db 61 ATCAACCATGACACACCATCATCTGGACAGAGGCTTACATGGACAGCCGGCTCTTCACA 120
Qy 435 SerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProValPheSerLysLys 454
Db 121 TCAGAGGCACAGAGCTGTATGCTCTCCACACAGTGGCCATGCTGTCTTCAGCAAAAAG 180
Qy 455 AsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAspValAlaLeuArg 474
Db 181 AATGAACAAGATCCCATGGCATTCCTCTGGGTGTAGTGGGCTCTGACGTGACCCCTAAGA 240
Qy 475 GluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyrAlaPheLeuAsn 494
Db 241 GAGCTCATGAAGCTGGCACCCCATATAAGCTTGGGGTGCATGGCTATGCTCTTCTTGAAC 300
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Qy 595 TyrIleLeuGlyAsnThrSerValGluGlyLeuHisAspLeuLeuHisProAsp 614
Db 601 TACATCTCTCTGGGGAACACATCTGTGGAAAGAGGCTGTGCACGACTTGTCTCATCCGGAT 660
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Qy 635 LeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAsp 649
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RESULT 12
BQ919363
LOCUS BQ919363
DEFINITION AGENCOURT_8779072 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6373010
5', mRNA sequence.
ACCESSION BQ919363
VERSION BQ919363.1 GI:223334061
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 940)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabe-remail.nih.gov
Tissue Procurement: DCTD/DTF/Gazdar
cDNA Library Preparation: Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM2549 row: 1 column: 03
High quality sequence stop: 524.

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            /lab_host="DH10B (phage-resistant)"
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            GGACGAG(G). Library constructed by Ling Hong in the
            laboratory of Gerald M. Rubin (University of California,
            Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
            Superscript II RT (Life Technologies). Note: this is a
            NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 5.64e-120 Length: 940
Score: 1208.00 Matches: 236
Percent Similarity: 83.62% Conservative: 4
Best Local Similarity: 82.23% Mismatches: 13
Query Match: 21.10% Indels: 34
DB: 5 Gaps: 3

US-09-833-222a-10 (1-1090) x BQ919363 (1-940)

Qy 787 AlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLysPheTTPAlaAlaThrArg 806
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Qy 807 GlnCysSerThrValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCys 826
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Db 139 TTCGTCTCGCAACAACAGGGTTCATTCGTATCTCCAGAGGTTCCCA----- 186
Qy 847 PheLeuGlyGluValAspGlyAlaValLeuThrGlnLeuSerMetGlyValPheSer 866
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Qy 867 Gln-ValThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisSerAl 886
Db 187 GAGAGTGACTATGATGACTATCAGGCGCATGTGCACACCCCTCGAGTCCACACAGTGC 246
Qy 886 aAlaGlnProLeuValSerProIleSerAlaPheLeuThrAlaThrArgTTPLeuGly 906
Db 247 AGCCAGCCCCCTGGTGCAGCCCAATTTCTGCTCTTTCAGCGCGCAGGTTGGTGTGCA 306
Qy 906 nGluLeuValLeuPheLeuLeuGluTTPSerValTTPGlySerTTPYrAspArgGlyAl 926
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Qy 926 aGluAlaLysSerValPheHisSerHisLysHisLysGlnAspProLeuGlnPr 946
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Qy 986 uLeuLeuValThrAspProThrCysAspCysSerIlePheProProValLeuGlnG 1006
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Qy 1006 uAlaThrGluValLysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLe 1026
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Qy 1026 uArgArgArgProAspSerCysHisAlaPheHisProGluValArgValGluAlaAsp 1046
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Db 787 TGGGGGGCTACTGCCCC 803

RESULT 13
BI908463
LOCUS BI908463
DEFINITION BI908463 777 bp mRNA linear EST 16-OCT-2001
ACCSSION BI908463
VERSION BI908463.1 GI:16171419
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/.
1 (bases 1 to 777)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabe-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LIAM11548 row: m column: 06
High quality sequence stop: 777.

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            cloning). Average insert size 1.7 kb, insert size range

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1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH MGC Library."

ORIGIN

Alignment Scores:				
Pred. No.:	2.43e-117	Length:	777	
Score:	1182.50	Matches:	233	
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Best Local Similarity:	84.12%	Mismatches:	12	
Query Match:	20.65%	Indels:	29	
DB:	4	Gaps:	2	
US-09-833-222A-10 (1-1090) x BI908463 (1-777)				
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DB	63	AGCACTGTGGATGGCGCGTGACACAGAGCTCGAGGACAGTATCTGGATCTGGATCTGCTC	122	
QY	829	IleAspAsnArgGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeu	848	
DB	123	ATCGACAAACACGGGTTCAATCTCTGATCTCCAAGAGGTCCCGA-----	164	
QY	849	GlyGluValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGln-Va	868	
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QY	888	nProLeuValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnIle	908	
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QY	908	uValLeuPheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAl	928	
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QY	988	uLeuValThrAspProThrCysAspCysSerIlePheProProValLeuGlnAlaAlaTh	1008	
DB	531	CCTGGTCACAGAGCCACCTGTGACTGTGAGCATCTTCCACACAGTGTGCAGGAGGCGAC	590	
QY	1008	rGluValLysTyraAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgAr	1028	
DB	591	AGAAGTCAAAATATAATCCCTCTGTCAAAATGTACCGGATGGCTCCCAAGAGTCCCGCG	650	
QY	1028	gArgProAspSerCysHisAlaPheHisProGluValArgValGluAlaAspArgGlyTr	1048	
DB	651	CGACACAGACTCTCTGGCAGCGCTTCCATCCAGAGGA-CGAATGCC-CAGGACTCGGCGG	708	
QY	1048	pAlaGlyPheSerSerProAsnPro-----LeuCysLeuGlyLeuCys	1062	
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RESULT 14

AK044603	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED	REFERENCE	AUTHORS	COMMENT
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Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

Retina RNA was provided by Dr. Stefano Gustincich (Department of
Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA
02115, USA) whose assistance is gratefully acknowledged. Please
visit our web site for further details.

URL:<http://genome.gsc.riken.jp/>
URL:<http://fantom.gsc.riken.jp/>.

CDS

mutative"

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Alignment Scores:

Alignment Scores:		
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DB:	3	Gaps: 44

US-09-833-222A-10 (1-1090) x AK044603 (1-3527)

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Oy	56	LeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArgArgLysValGlu	75
Db	351	CAGAAAATTGCTGGAGAAAGTGGCAGGGGACATCGAGACCTGCTGGACAGGAAGTCCAG	410
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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Title: US-09-833-222a-10
Perfect score: 5726
Sequence: 1 MAVALGTRRRDRVKLWADTF.....MPMNTVPVLLGGNIRVYAL 1090

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: piri.*
2: piri2.*
3: piri3.*
4: piri4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3422	59.8	1091	2 T30256	calcium channel al
2	1089	19.0	1106	1 CHRB2	calcium channel pr
3	1077.5	18.8	1091	2 JH0565	calcium channel al
4	1056.5	18.5	1091	2 A44147	calcium channel pr
5	638.5	11.2	734	2 S44617	CSOC3.11 protein -
6	543	9.5	1148	2 T18770	probable calcium c
7	209.5	3.7	1450	2 C86880	hypothetical prote
8	175	3.1	946	1 IYHU2	inter-alpha-trypsi
9	172.5	3.0	946	2 JC5575	inter-alpha-trypsi
10	166.5	2.9	946	2 S54354	inter-alpha-inhibi
11	164.5	2.9	930	2 JC5368	inter-alpha-trypsi
12	150.5	2.6	889	2 JC5576	inter-alpha-trypsi
13	148.5	2.6	886	2 S54355	inter-alpha-trypsi
14	146.5	2.6	885	2 S30350	inter-alpha-trypsi
15	145.5	2.5	2819	2 A90551	conserved hypotet
16	144.5	2.5	921	2 JC4625	inter-alpha-trypsi
17	144	2.5	820	2 AD2357	hypothetical prote
18	144	2.5	1091	2 C95133	exonuclease RexB
19	144	2.5	1091	2 G98001	second chain of ma
20	143	2.5	655	2 S59836	hypothetical prote
21	142	2.5	911	2 A39967	inter-alpha-trypsi
22	140.5	2.5	570	2 AC2356	hypothetical prote
23	135.5	2.4	676	2 T47637	hypothetical prote
24	135	2.4	436	2 E90261	hypothetical prote
25	134.5	2.3	1276	2 S11455	botulinum neurotox
26	134.5	2.3	1329	2 AE1901	WD-repeat containi
27	134	2.3	1073	2 S14032	kinesin-related pr
28	132.5	2.3	918	2 E90542	lipoprotein [impor
29	131.5	2.3	2280	2 T38906	acetyl-CoA carboxy

30	131	2.3	1085	2 T38378	kinesin-like prote
31	129.5	2.3	587	2 I64023	hypothetical prote
32	129.5	2.3	906	2 D82899	alanyl-tRNA synthet
33	129.5	2.3	1188	2 F64367	pyruvate, water di
34	129	2.3	802	2 C90326	hypothetical prote
35	129	2.3	932	2 JC5953	inter-alpha-inhibi
36	129	2.3	8243	2 T31307	type I fatty acid
37	128	2.2	689	2 F84811	probable retroelem
38	128	2.2	914	2 JC5574	inter-alpha-trypsi
39	127.5	2.2	709	2 AD2843	methyl-accepting c
40	127.5	2.2	717	2 E97620	methotactic trans
41	127	2.2	629	2 C83107	chemotactic trans
42	126.5	2.2	1411	2 S55123	hypothetical prote
43	126.5	2.2	2279	2 T42531	acetyl-CoA carboxy
44	124.5	2.2	885	2 AB1944	ferrichrome iron r
45	123.5	2.2	2670	2 T37919	GCN1 homolog - fis

ALIGNMENTS

RESULT 1

T30256
calcium channel alpha-2-delta-C chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30256
R:Klugbauer, N.; Lacinova, L.; Marais, E.; Hobom, M.; Hofmann, F.
J. Neurosci. 19, 648-691, 1999
A:Title: Molecular diversity of the calcium channel alpha2delta subunit.
A:Reference number: Z20794
A:Accession: T30256
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1091 <KLU>
A:Cross-references: UNIPROT:Q9Z1L5; EMBL:AJ010949; PIDN:CAA09423.1
A:Experimental source: brain
C:Superfamily: calcium channel alpha-2 chain

Query Match	59.8%	Score	3422;	DB 2;	Length	1091;
Best Local Similarity	60.0%	Pred. No.	1.5e-217;			
Matches	627;	Conservative	188;	Mismatches	212;	Indels 18; Gaps 6;
Qy	13	VKLWADTFGGDLVNTVTKYSGSLLQLKKYKDVSSLLKIEVDGLLEVRKSEDMENLMRR	72			
Db	42	VKLWASAFGGEIKSIAAKYSGSLLQLKKYKEYEKDVAIEIDGLQVLKLAIMEEMFHK	101			
Qy	73	KVEAVQNLVEAAEADLNHEFNESSLVFDYVNSVLINERDEKGNFVEIGAELLESNAHFS	132			
Db	102	KSEAVRRLVEAAEAAHLKHEFDADLQYEFNAVLINERDKGNFLEUGKEFILAPNDHFN	161			
Qy	133	NLPVNTSISVQLPTVYNNKDPDILANGVYVNSEALNAVVFENFORDPTLTWQYFGSATGFF	192			
Db	162	NLPVNTSLSDVQVPTNMYNKDPAIVGVYVSWESLNVKVFVDFNDRDPSLIWQYFGSANGFF	221			
Qy	193	RIYPGIKWTPDENGVTFFDCNRNGWIQAATSPKDVILVDVSGSMKGLRWIAKHTITT	252			
Db	222	QYPGIKWEPDENGVIATFDCNRNRKWIQAATSPKDVILVDVSGSMKGLRTIAKQTVSS	281			
Qy	253	ILDTLGENDFVNIIAANDYVHYIEPCFKGLVQADRNRHEFKLLVBEELWVGVVVDQA	312			
Db	282	ILDTLGDDDDFFNITTYNEELHYVEPCNLGTLVQADRNRKHEHLEHDKLFAKIGMLDIA	341			
Qy	313	LREAFQILKQFQBAKQSLCNQAIMLISDGAVDYEPVEFKYVNPDCQKRVFTYLIQREV	372			
Db	342	LNFAFNILSDFTNGTGGISCSQAIMLITDGAVDYDTIFAKYVNPDRKRVFTYLIQREA	401			
Qy	373	SPADRMKWIACNNKGYTYTISTLADQENVMYHLVSRPMVINHDHDIITWEAYMOSKL	432			
Db	402	AFADNLKWMACANKGPFQTYTISTLADQENVMYHLVSRPMVINHDHDIITWEAYMOSKL	461			
Qy	433	LSSQA----QSLTLLTTVAMPVFSKNETSHGILLGLGVSDVALRELMLKAPRYKLGVH	488			

Db 462 POAQLDADQGLVMTTVAAMPVFSQNETRSKGIILGVGVGTDPVVKSLLTIPKYKLGIIH 521

Qy 489 GYAFINTNNGYILSHPLDLPLRYRGKKLPKPNYNSVDLSVEWEDQAESLRTAMINRET 548

Db 522 GYAFINTNNGYILTHPELPLRYEGKK-RRKPNYSSVDLSVEWEDRDDVLRNANVRKT 580

Qy 549 GTLSMDVKVPMDKGRVLFITNDYFTDIIDTDFSLGAVLSRGHGEYILLGNTSVESGLH 608

Db 581 GKFSMEVKTKVDKGRVLMNTDYYTDIKGTPFSLGVALSRGHGKYFFRGVNTVIEBGLH 640

Qy 609 DLLHPDLALAGDWIYCTIDDPDRHKLSQLAMIRFTRKDPDLCEDEBELVREVLDAVV 668

Db 641 DLEHPDVLADWYSYNTDLHPEHILSLQLEAIKLYLKGKEPLQCDKELIQEVLDAVV 700

Qy 669 TAPMEAWTALALNMSSEHVDMAFLGTRAGLLRSSLFVSGEKVSDRKLTPDEASV 728

Db 701 SAPLEAWTALNKSNSDKGEVAFGLGTRGLSLRNLNLFVGAELTNQDFLKGADKENI 760

Qy 729 FTLDLRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVATVDKRTATAAAA 788

Db 761 FNADHFLWYRRAAEQIAGSFVYSIPSTG-TVKNVNVVTAFTSIQLLDERKSPVVAAV 818

Qy 789 GVQMKLEFLQKFWAATROQSTVDGPTQSCEDSDLCFVIDNNGFFILISKRETRGRFL 848

Db 819 GIOQMKLEFFQKFWAATROQSTVDGPTQSCEDSDLCFVIDNNGFFILISKRETRGRFL 878

Qy 849 GEVDGAVLTOLLSMGVFSQVMTDYQAMCKPSSHHSAAQPLVSPISAFLTATRWLLOEL 908

Db 879 GEVEGAVMKNLLTWGSEFKRITLDYQAMCRANKESSDSANGLDLPYKAFLSAAKNMTEL 938

Qy 909 VLFELEWVMSGYDWRGAESAQSVFHHSHGHKQDPLQPCDTEYFVYQYPAIREANGIVE 968

Db 939 VLFELEWVMSGYDWRGAESAQSVFHHSHGHKQDPLQPCDTEYFVYQYPAIREANGIVE 990

Qy 969 CGPCQKVFVVOQIPNSNLLLVITDPTCDSCIFPPVQLEATEVKYNASVKCDMRSKLRR 1028

Db 991 CEDCSKSFVQQIPSSNLLLVITDPTCDSCIFPPVQLEATEVKYNASVKCDMRSKLRR 1050

Qy 1029 RPDSCFAPHPVEVRVADRGWAGFSS 1053

Db 1051 RPESCHGFPE---ENARECGGASS 1072

RESULT 2

CHRB2

calcium channel protein alpha-2 chain precursor - rabbit

N;Alternate names: dihydropyridine-binding protein, 140K

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 31-Mar-1992 #sequence revision 31-Mar-1992 #text_change 09-Jul-2004

C;Accession: S10579; A39518; A33409

R;Ellis, S.B.; Williams, M.E.; Ways, N.R.; Brenner, R.; Sharp, A.H.; Leung, A.T.; Campbell, S.C. 1998

A;Title: Sequence and expression of mRNAs encoding the alpha(1) and alpha(2) subunits of the dihydropyridine-sensitive calcium channel

A;Reference number: S10579; MUID:88336904; PMID:2458626

A;Accession: S10579

A;Molecule type: mRNA

A;Residues: 1-1106 <ELL>

A;Cross-references: UNIPROT:P13806; EMBL:M21948; NID:g164762; PIDN:AAA81562.1; PID:g164762

A;Note: 57-Asn, 106-Lys, and deletion of 620-Ser were also found

R;Jay, S.D.; Sharp, A.H.; Kahn, S.D.; Vedvick, T.S.; Harpold, M.M.; Campbell, K.P. J. Biol. Chem. 266, 3287-3293, 1991

A;Title: Structural characterization of the dihydropyridine-sensitive calcium channel

A;Reference number: A39518; MUID:91131638; PMID:1847144

A;Accession: A39518

A;Molecule type: protein

A;Residues: 961-973 <JAY>

A;Note: this sequence represents the amino end of a glycosylated peptide that appears at the amino end and identical molecular weights (17K) following deglycosylation

R;Hamilton, S.L.; Hawkes, M.J.; Brush, K.; Cook, R. Biochemistry 28, 7820-7828, 1989

A;Title: Subunit composition of the purified dihydropyridine binding protein from skeletal muscle

A;Reference number: A33409; MUID:90122765; PMID:2558113

A;Accession: A33409

A;Status: preliminary

A;Molecule type: protein

A;Residues: 27-44, 'S', 46-47 <HAM>

C;Superfamily: calcium channel alpha-2 chain

C;Keywords: calcium; disulfide bond; glycoprotein; ion channel; membrane protein; phosphatase

F;1-26/Domain: signal sequence #status predicted <SIG>

F;27-1106/Product: calcium channel alpha-2 chain #status predicted <MAT>

F;94,138,186,326,350,470,477,606,615,678,697,784,827,891,898,988,1001,1081/Binding site:

Query Match 19.0%; Score 1089; DB 1; Length 1106;

Best Local Similarity 28.0%; Pred. No. 2e-63;

Matches 315; Conservative 222; Mismatches 431; Indels 156; Gaps 44;

Qy 13 VKLWADTFGDLVNTVTYKSGSLLLQKKYKDVSSLLKIBEVDSGLVLRKFSDEMNLRR 72

Db 35 IKSWDKMQEDLVTLAKTAGVGHQVLDIYEKYODLYTVFPPNARQLVETIARIDIELLSN 94

Qy 73 KVEAVQNLVEAAEADLNHEFNESLVD---YNSVLINERDEKGNFVELGAE-----FL 124

Db 95 RSKALVRLALEAEKVQAAHQWREDFASNEWVYNAK--DDLDPKNDSEBGSQRIKPVFI 152

Qy 125 LLSNAHFSNLPVNTSSVQLPTNVYKDPDILNGVYMSALNAVFNVPORPDTLTWQY 184

Db 153 DDAAN---FRQVSYQHAHVHIPTDIYEGSTIVLNELNWTSALDDVFKQREEDPSLLQV 209

Qy 185 FGSATGFFRIYPGIKWTPDE---NGVITFCRNRGWYIQAAATSPKDIKIVLDVDSGSMKGL 241

Db 210 FGSATGLARYYPASPMVDSNRTPNKIDLDVRRRPWYIQGAASPKDMLILVDVSGVSG 269

Qy 242 RMTAKHTITTLDTLGENDFVNI IAYNDYVHYIEPCFKGILVQADRDNRHFKLLVVEL 301

Db 270 TLKLI RTSVSEMLETLSDDDFNVASFNSAQDVS-CFQH-LVQAVNRKKVLKDAVNI 327

Qy 302 MKVGVDVQALREAFQILKQEAQKQSLCNQAIIMLSDGAVDEYEPFEKYNWDCVK 361

Db 328 TAGKITDYKKGFSFAPEQLNLNVNVRAN--CNKIIMLFTDGGEEAQAEIFAKYN-KDKKV 384

Qy 362 RVFTYILIGREVSFADRMKWIACNNKGYTQISTLADTQENVMVYLHLVSRPMVNH--H 419

Db 385 RVFTSVGQHYNDRGPIQWACENKGYEIEISGAIRINTQEIYLDVLRPVMVLAGDKAK 444

Qy 420 DIITWYANMDSKLLSSQAQSLTLLTTVAMPVFS---KKNETR-SHGILLGVVGSVAUR 474

Db 445 QVQWNTNVYLD-----ALELGLVITGTLFVFNITQGFENKTNLKNQLILGVMGVDVSL 497

Qy 475 ELMKLAPRYKLGVGHYAFNLNNGYILSHPLRLPLYRECKL-----KPKENYN- 523

Db 498 DIKRLTPRFLPCNGYFAIDPNGYVLLHPNIDP-----KPIGVGIPITNLKRRRPNVQN 552

Qy 524 -----SVDLSEVEWEDQAE-SLRATAMINRETGTLSMDVKVP-----MDKGRVLF 569

Db 553 PKSQEPVTLDFLDLAELNDIKVEIRNKMIDGESGEKFTFLVKSQDERYIDKGNRT- 608

Qy 570 NDYFTDISDTPFSLGAVLSRGHGEYL---LGNTSVEEGLHDLHPD-----LALAGD 620

Db 609 --YTWTVPNGTDYSSIALVLPTYSFVYIKAKIETITQARYSETLKPDNFEESGYTFLAP 666

Qy 621 WYCYCTDIDPDHRLKSQLEAMIRFLTRKDP-DLECDDELAVREVLDAVTPM-EAYWTA 678

Db 667 RQYC-SDLKPSDNNTTEFLNFNNEFIDRKTTPNPNSCNTDLINRVLLDAGFTNELVQWYS- 724

Qy 679 LALNMSSEHVVVDWMAFLGTRAGLLRSSLFVSGEKVSDRKLTPDEASVFTLDRPPLWY 738

Db 725 -----KQNKIKGVKARFVVTDCGIR---VYPKEAGENWQENPEYEDSF-----Y 767

Qy 739 RQASEHPAGSFVFNLRW---AEGPESAGEPMVVTASTAVATVDVKRTATAIAAAGVQMKLEF 796

Db 768 KRSLDN--DNYVFTAPYFNKSGFGAYESGIMV--SKAVEIYIQGKLLKPAVVGIKIDVNS 823

Qy 797 LQKFWAAATRO--CSTVDGPTYQSCEDSD-LDQCFVIDNNGFTILISKR---SRETGRFLGE 850

Db 824 WIENFTKTSIRDPCA---GPVCDCKRNSDVMDCVILDDGGFLLMANHDDYTQIGRPFGE 880

Qy 851 VDGAVALTQLSMGVPSQVMTYDQAMCKP-----SSHHSAAQPLVS-----PISAFITAT 901
 Db 881 IDPSLMRHLNINISYAFNKSVDYQSVCEGAPKQAGHRSAYVPSIADILQIGWATAA 940
 Qy 902 RW-LLOELVLFLLEWSVMGSDYRGAASVFFHSHKHKKDPL-----QPCDTEYVVF 954
 Db 941 AWSILOQFLSLT-----FPLLEADN-----EDDFTASMSKQSCITEQTQY 984
 Qy 955 VYQPAIRANGIVEGCPQKVFVVOQIPNSNLLLVLPD--TCDCSIFPPVLOBATEVKY 1012
 Db 985 FFDNDSKFSGLVDCGNCRIFFHVEKLMNTNLIIFIMVESKGTCPDCTRLLIQAOTS--- 1041
 Qy 1013 NASVKCDRMSQKLRRRPSDCHAFHPEVRVADRGWAGFSSPNP 1056
 Db 1042 DGPDPDMVKQPRYKGPVDC--FDNNV-LEDYTCGGVSGLNP 1082

RESULT 3
 JH0565
 calcium channel alpha-2b chain precursor - human
 C:Species: Homo sapiens (man)
 C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C:Accession: JH0565
 R:Williams, M.E.; Feldman, D.H.; McCue, A.F.; Brenner, R.; Velicelebi, G.; Ellis, S.B.;
 Neuron 8, 71-84, 1992
 A>Title: Structure and functional expression of alphas, alpha2, and beta subunits of a r
 A:Reference number: JH0564; MUID:92110010; PMID:1309651
 A:Accession: JH0565
 A:Molecule type: mRNA
 A:Residues: 1-1091 <WIL>
 A:Cross-references: UNIPROT:P54289; GB:M76559; NID:g179761; PIDN:AAA51903.1; PID:g179762
 A:Experimental source: basal ganglia
 A>Note: Several conflicts are found between GenBank submission, authors' translation in
 C:Comment: This protein is a subunit of the voltage dependent calcium channel.
 C:Superfamily: calcium channel alpha-2 chain
 C:Keywords: glycoprotein, phosphoprotein
 F;1-24/Domain: signal sequence #status predicted <SIG>
 F;25-1067/Product: calcium channel alpha-2b chain #status predicted <CAL>
 F;32,268,326,539,635,1087/Binding site: phosphate (Thr) (covalent) (by protein kinase C)
 F;91,142,250,625,817/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #sta
 F;92,136,184,324,348,468,475,594,663,682,769,812,876,883,973,986/Binding site: carbo
 F;501/Binding site: phosphate (Thr) (covalent) #status predicted
 F;833/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predic

Query Match 18.8%; Score 1077.5; DB 2; Length 1091;
 Best Local Similarity 28.3%; Pred. No. 1.1e-62;
 Matches 315; Conservative 217; Mismatches 432; Indels 151; Gaps 44;

Qy 13 VKLMADTFGGDLVNTVTKYSGSLLLQKKYKDVESLKIIEVDGLLELVKFSDEMMLRR 72
 Db 33 IKSVDRKMQEDLVTLAKTASGVNLVDIYEKYQDLYTVEPNARQLVEIAARDIEKLLSN 92
 Qy 73 KVEAVQNLVEAAEADLNHERNESLVPD---YNSVLINERDEKGNFVELGAE-----FL 124
 Db 93 RSKALVSLALEAEKVAQAQHMREDFASNEVVYNAK--DLDLPKNDSEPGSRIKPVFI 150
 Qy 125 LESNAHPSNLPVNTSISVOLPTVYVYKNDPDLNGVYMSALNAVVENFQDPTLLTQY 184
 Db 151 EDAN---FGRQISVQHAHVPTDIYEGSTIVLNELNWTLSALDEVFKKNEEDPSLLMQV 207
 Qy 185 FGSATGFRFYPIGKWTPTDE---NGVITFCRNGWTYQIATSKDVLIVDVSGSMKGL 241
 Db 208 FGSATGLARYYPASPVDNRSRTPNKIDLYDVRPRPWTYQGAASPKDMLILVDVSGSVSGL 267
 Qy 242 RMTAKHTITITLDTLGENDPVNIAYNDVHYIETPCFKGLVQADRDNRHFKLLVEEL 301
 Db 268 TLKIRIVSSEMLTSLDSDFPVNASFNSNAQDVS-CFQH-LVQANVRNKKVLKDAVNI 325
 Qy 302 MVKGGVVDQALREAFQILKQFQBAKQGLCNQAIMLISDGAVDYBPFVEKYNWPPCKV 361
 Db 326 TAKGITDYKKGFSFAFQOLLNYSVRAN--CNKIIMLFTDGEERAQEIFNKYN-KDKKV 382
 Qy 362 RVFTYTLIGREVSFADRMKWIACNNKGYTQISTLADTQENVMYHLVLSRPMVINHD--H 419

Db 383 RVFRFSVQGHNYRGPQIOMACENKGYEIPSGAIRINTQEQYLDVLGRPMVLGAKAK 442
 Qy 420 DIITWETAYMDSKLLSSQAQSLTLLTTVAMPVFS-----KQNETR--SHGILLGVGSDVALR 474
 Db 443 QVQWTVNYLD-----ALEGLVITGTLVFNITGQFENKTNLKNOLLGVMGVDVSL 495
 Qy 475 ELMKLAPRYKLVGHVAFNLNNGYILSHDPLRLPYREGKKLKPKNVNSVDLSEVWEED 534
 Db 496 DIKRLTPRFTEPCNGYFAIDPNGYVLLHFNLPQ--KNPKSQEPV---TLDFDLDAELEN 549
 Qy 535 QAB-SLRATAMINRETGLSMDVKVP-----MDKGEVLFLTNDYFPTDTSIDTSPFSLGAV 587
 Db 550 DIKVEIRNKMIDGESGEKTRTLVKSODERYIDKGNRT-----YTPVNGTDTYSLALV 603
 Qy 588 LSRGHGEYILLGNTSVBEGE-----HDLHPD-----LALAGDWIYCIITDID 629
 Db 604 LPTYSFYI---KAKLEETITQARSKKGMKDSSETLKPDPNFESSGYTFIAPRDYC-NDLK 659
 Qy 630 PDHRKLSQLEAMIRFLTRKOP-DLEDEELVREVLFDVAVTAPM-EAYWTALALNMSEES 687
 Db 660 ISDNTEFFLLNFNEFIDRKTNNPNCNADLINRVLLDAGFTNELVQNYWS-----KQKN 713
 Qy 688 EHVDVMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPPEDEASVFTLDRFPLWYRQASEHPAG 747
 Db 714 IKGVKARFVVTDDGITR---VYPKEAGENWQENPETYEDSF-----YKRSLDN--D 759
 Qy 748 SFVFNLRW--AEGPESAGEPMVVTASTAVATVTKRTAIAAAGVQVMKLEFLQKFWAAT 805
 Db 760 NYVFTAPYFNKSGPAGYESGMV--SKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTS 817
 Qy 806 RQ--CSTVDGPTYQSCEDSD-LQCFVIDNNGFILIISKR-----SRETGRFLGVDGAVITQL 859
 Db 818 IRDPFCA---GPVDCCKRNSDVMCDVILDDCGFLLMANHDDYTNQIGRFFGEBIDPSLMRHL 874
 Qy 860 LSNMGVFSQVMTYDQAMCKP-----SSHHSAAQPLVS---PISAFITATRW-LLOELV 909
 Db 875 VNLISVAFNKSVDYQSVCEGAPKQAGHRSAYVPSVADILQIGWATAAAMSILOQFL 934
 Qy 910 LFLLEWSVMGSDYRGAASVFFHSHKHKKQDPL-----QPCDTEYVFPVYQPAIREA 963
 Db 935 LSLT-----FPLLEAVEM-----EDDFTASLSKQSCITEQTQYFPDNDKSF 978
 Qy 964 NGIVEGCPQKVFVVOQIPNSNLLLVLPD--TCDCSIFPPVLOBATEVKYNVSKVCDRM 1021
 Db 979 SGVLDCGNCRIFFHVEKLMNTNLIIFIMVESKGTCPDCTRLLIQAETSQDGN---PCDMV 1035
 Qy 1022 RSQKLRRRPSDCHAFHPEVRVADRGWAGFSSPNP 1056
 Db 1036 KQPRYKGPVDC--FDNNV-LEDYTCGGVSGLNP 1067

RESULT 4
 A44147
 calcium channel protein alpha-2 chain precursor - rat
 N;Alternate names: dihydropyridine-sensitive L-type
 N;Contains: calcium channel alpha-2 chain
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
 C;Accession: A44147
 R;Kim, H.L.; Kim, H.; Lee, P.; King, R.G.; Chin, H.
 Proc. Natl. Acad. Sci. U.S.A. 89, 3251-3255, 1992
 A;Title: Rat brain expresses an alternatively spliced form of the dihydropyridine-sensit
 A;Reference number: A44147; MUID:92228762; PMID:1314383
 A:Accession: A44147
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1091 <KIM>
 A:Cross-references: UNIPROT:P54290; GB:M86621; NID:g203954; PIDN:AAA41088.1; PID:g203955
 C;Superfamily: calcium channel alpha-2 chain
 C;Keywords: calcium; glycoprotein; ion channel; transmembrane protein

Query Match 18.5%; Score 1056.5; DB 2; Length 1091;

JC5575
inc α -trypsin inhibitor heavy chain 2 - golden hamster
C/Species: Mesocricetus auratus (golden hamster)
C/Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 09-Jul-2004
C/Accession: JC5575; PC4485

QY 225 PKDIVILVDVSGSMKGLRMTIAKHTITTTILDITLGENDFVNI IAYNDYVHYI

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Db 308 PKNLFVIDVSGSMGKMKQVTQAEAMKTIILDLRTDQFSVDNFHNR-----TWNDIV 363
QY 285 QARDNRHFKLLVEELMVGVGVVDOALREAFQILKQFOEAKQGSCLN-----QAIMLIS 340
Db 364 SATKQTADAKRYIEKIQPSGGNINEALLRAIFIL---NEASNMGLLNPDVSLIILVS 420
QY 341 DG-----AVEDYEPVFEKYNWPCCKVRVFTYVLIGREVSFADRMKWA 382
Db 421 DGPFTVGLKSLKIQKVKQSIQD-----NISLFSLGIGFDVY-DFLKRLS 466
QY 383 CNKNGYVQIISTLADQENYMEYHLVSRPMVIN-----HDH-----D 420
Db 467 NENRGIAQRIYGNQDTSSQLKFKVQVSTPLLRNVQPNYPQASVTDVTQNNFHNFGSGE 536
QY 421 IINTEAMWDSKLLSSQAQSLTLTT 445
Db 527 IVVAGKFDPSKL--TEVQSIITATS 549

RESULT 11
JX0368
inter-alpha-trypsin inhibitor heavy chain-related protein precursor - human
N;Alternate names: IHRP; Plasma glycoprotein
C;Species: Homo sapiens (man)
C;Date: 22-Apr-1995 #sequence revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: JX0368; PID:9523915; S78548
R;Saguchi, K.; Tobe, T.; Hashimoto, K.; Sano, Y.; Nakano, Y.; Miura, N.H.; Tomita, M.
J. Biochem. 117, 14-18, 1995
A;Title: Cloning and characterization of cDNA for inter-alpha-trypsin inhibitor family H
A;Reference number: JX0368; MUID:9523915; PMID:7775381
A;Accession: JX0368
A;Molecule type: mRNA
A;Residues: 1-930 <SAG1>
A;Cross-references: UNIPROT:Q14624; DDBJ:D38595; NID:g664887; PID:BAA07602.1; PID:g1483
A;Accession: PC2355
A;Molecule type: protein
A;Residues: 29-44; 48-55; 61-75; 99-111; 140-151; 163-169; 211-224; 246-267; 274-281; 296-329; 392
A;Experimental source: liver
R;Nishimura, H.; Kakizaki, I.; Muta, T.; Sasaki, N.; Pu, P.X.; Yamashita, T.; Nagasawa,
FEBS Lett. 357, 207-211, 1995
A;Title: cDNA and deduced amino acid sequence of human PK-120, a plasma kallikrein-sensi
A;Reference number: S68457; MUID:95104473; PMID:7805892
A;Accession: S68457
A;Molecule type: mRNA
A;Residues: 1-84, 'I', 86-113, 'S', 115-930 <NIS>
A;Cross-references: EMBL:D38535; NID:g624879; PID:BAA07536.1; PID:g1402590
A;Accession: S78548
A;Molecule type: protein
A;Residues: 29-45; 171-184; 211-239; 274-281; 301-315; 429-443; 488-502; 690-695; 697-700; 703-72
A;Experimental source: liver
C;Comment: The amino-terminal 600 residues exhibits homology with those of inter-alpha
C;Function:
A;Description: highly sensitive to plasma kallikrein
C;Superfamily: inter-alpha-trypsin inhibitor complex component II
C;Keywords: chondroitin sulfate proteoglycan; glycoprotein; serine proteinase inhibitor
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-697/Product: inter-alpha trypsin inhibitor heavy chain-related protein #status pred
F;688-930/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;81,207,517/Binding site: carbohydrate (Aan) (covalent) #status predicted
F;666/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted
F;696,702/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;701/Binding site: carbohydrate (Thr) (covalent) #status predicted

Query Match 2.9%; Score 164.5; DB 2; Length 930;
Best Local Similarity 19.0%; Pred. No. 0.017;
Matches 147; Conservative 118; Mismatches 313; Indels 195; Gaps 31;

QY 26 NTVTKYSGSLLOKQYKDVESLUKIEVDGLVLRKFSF-----DNENML 70
Db 62 NTVQEAATFQWELPKKAFITNFSWNIDGMYPGIIEKAAQAQYSAVAKGKAGLVKAT 121
QY 71 RRKVEAVQNLVEAAEADLNHEFNESLVFDYDYNVSLINERDEKGNFVELGAEFLLSENAH 130

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Db 122 GRNMEQFOYSVSVAPNAKITFE-----LVYE-----ELLKRR-----LGVYELL----- 160
QY 131 FSNLPNTSISSVOLPTNVNKKDPDILNGVYMEALNAVVFENFQRPDPTLTWQYFGSATG 190
Db 161 ---LKVRPQOLVKHLQMDIHIFEP---QGISFLET-ESTFMTNQLVDALTWQ--NKTKA 211
QY 191 FRRIYPGI-----KWTDPDENGVIITFDCR-----NRGWYIQ-----AATS 224
Db 212 HIRFKRTLSSQKSPQQTVDGNLIIRYVDVRAISGSGIQENGIVFYHFAPEGUUTM 271
QY 225 PKDIVILVDVSGSMKGLRMTIAKHITITLDTLIGENDFVNIIAYNDVYHIEBCEKGLV 284
Db 272 PKNVFVIDKSGSMGRKIQOTREALIKILLDLSPRDQFNLIIVFSTEATQWRES---LV 327
QY 285 QARDNRHFKLLVEELMVGVGVVDOALREAFQIL---KQFOEAKQGSCLNQAIMLISD 341
Db 328 PASAENVNKAASFAGIQALGGTININDAMLMAVQLDSSNQEERLPEGSV--SLIILLTD 385
QY 342 G--AVEDYEPVFEKYNWPCD---KVRVFTYVLIGREVSFADRMKWAICNNKGYVTOISTLA 396
Db 386 GPTVGETNPRSIQNNVREAVSGRYSIFCLGFGFDVSYAFLEK-LALDNGGLARRIHEDS 444
QY 397 DTQENYMEYHLVSRPMVINHDHDIITWYAYMDSKLLSSQAQSLTLTTTVAMPVFSKNE 456
Db 445 DSALQLQDFYQEVANELL-----TAVTFEYPSNAVEEVTONNFRLLFKGSEMVVAGLKQ 498
QY 457 TRSHGILLGVG-----SDVALRELMLKLAAPRY-----KLGVH----- 488
Db 499 DRGPDVLTATVSGKLPTQNTITQTESVAEAEFQSPKYIFHNFMERLWAYLTIOQLLE 558
QY 489 -----GYAFLTNNGVILSHPD-----LRPL----- 509
Db 559 QTVSASDAQQAALNQALNLSLAYSVTPLTSMVVTKPDQEQSQVAEKPMEGESNRNV 618
QY 510 -----YREGKKL-KPKPNYNSVDLSEWEQAESLRTAMINRETGTL---MDVK 556
Db 619 HSGSTPFKYVLQCAKIPKEASFS---PRRGWNRQAGAAGSRM-NFRPGVLSRQLGLP 673
QY 557 VPMDKGKRVLFTNDYFFDDISDTPSLGAVLSRGHGEVILLGNTSVBEGHLHLLHPD-- 614
Db 674 GPPDPVDDHAAY---HPFRRLAILPASAPPATSNPDPAVSRVMNMKIEETMTTQTAPPI 729
QY 615 -----LALAGDWIYCIITIDPDHRLKLSQLEAMIRFLTRKDPDLECEELVRE 661
Db 730 QAPSAILPLPGOSVERLC-VDPHRR-----QGPVNLSDPEQGVETGQYERE 776

RESULT 12
JCS576
inter-alpha-trypsin inhibitor heavy chain 3 - golden hamster
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 17-Mar-1999
C;Accession: JCS576; PC4486
R;Nakatani, T.; Suzuki, Y.; Yamamoto, T.; Sinohara, H.
J. Biochem. 122, 71-82, 1997
A;Title: Molecular cloning and sequencing of cDNAs encoding three heavy-chain precursors
sin inhibitor heavy chain family.
A;Reference number: JCS574; MUID:97420688; PMID:9276673
A;Accession: JCS576
A;Molecule type: mRNA
A;Residues: 1-889 <NAK>
A;Cross-references: DDBJ:D89287
A;Experimental source: liver
A;Accession: PC4486
A;Molecule type: protein
R;Residues: 34-53; 449-475; 509-526 <NA2>
C;Comment: In the plasma three inter-alpha-trypsin inhibitor heavy chains 1, 2 and 3 were
that the complexes play important role for pancreatic cancer.
C;Superfamily: inter-alpha-trypsin inhibitor complex component II
F;236-239; 664-865/disulfide bonds: #status predicted

Query Match 2.6%; Score 150.5; DB 2; Length 889;

```


F:647/Modified site: chondroitin sulfate ester carboxyl end (Asp) (in mature form) #stad		
Query Match	2.6%; Score 146.5; DB 2; Length 885;	
Best Local Similarity	21.9%; Pred. No. 0.24;	
Matches	73; Conservative 63; Mismatches 147; Indels 51; Gaps 14;	
QY	118 ELGAEFLLENAHPSNLPUTNTSSVOLPTNVTYKDPDIL--NGVYSEALNAVVENFQ 175	
DB	149 ELTYEELK--RHKGKYTEMLKVPQKLVKH-PBIEVDIFEPQIGISMLDA-EASFITNDL 204	
QY	176 RDPTLTWQYFGSATGPFRIYPIGKWTPE-----NG-VITEPCRN----- 214	
DB	205 LGSALT-KSFSGKGHVSFPLS-----DQORSCPTCTDLSLLGDTITYDNRRESPNVQ 259	
QY	215 --RGWYIQ-----AATSPKDIVILVDVSGSMGLRMTIAKHTTTITLDTLGENDFVNII 266	
DB	260 IVNGYFVHFPAQGLPVVKNVAFVIDISGMAGRKLEQTKEALLRILEDMQBEDYLNFI 319	
QY	267 AYNDYVHYIEPCFGIILVQADRONREHFKLLVELLMVKGV-GVVDAQALREAFQILKQOE 325	
DB	320 LFSGDV---STWKEHLVQATPENLQBAKTFVKSMEDKGMTNINDGILLGISMINKAREE 375	
QY	326 AKQSLCNQAIMLISDGAVEDYEPVFEKY-----NWPDCVKRVFTYILIGREVSFADRMKW 380	
DB	376 HRIPERTSIVIMLTDGANVGSRSPEKIOENVRNAIGGRFPLYNLGFGNNLAY-NPLEN 434	
QY	381 IACNKGYYTQISTLADTQENVMYHLVLSRPV 414	
DB	435 MALENHGFARRIYEDSDADLQLQGFYEEVANPLL 468	
RESULT 15		
A90551		
conserved hypothetical protein MYPV_3130 [imported] - Mycoplasma pulmonis (strain UAB CT		
C;Species: Mycoplasma pulmonis		
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004		
C;Accession: A90551		
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Sanson, D.; Galisson, F.; Moszer, I.;		
Nucleic Acids Res. 29, 2145-2153, 2001		
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm		
A;Reference number: A99512; MUID:21267165; PMID:11353084		
A;Accession: A90551		
A;Status: preliminary		
A;Molecule type: DNA		
A;Residues: 1-2819 <KUR>		
A;Cross-references: UNIPROT:Q98Q98; GB:AL445566; PID:g14089727; PIDN:CAC13486.1; GSPDB:G		
A;Experimental source: strain UAB CTIP		
C;Genetics:		
A;Gene: MYPV_3130		
A;Genetic code: SGC3		
Query Match	2.5%; Score 145.5; DB 2; Length 2819;	
Best Local Similarity	18.7%; Pred. No. 1.9;	
Matches	154; Conservative 130; Mismatches 261; Indels 279; Gaps 41;	
QY	41 YKDVESSLKIEEVDGLLEVRK----FSEDMMNLMRRKVEAVQ--NLVEAAEEADLN-HEF 93	
DB	733 FYEVSKTL-VNIVDTLELLEKVLKNFIEEIKSSAQLKLSNPKFENLIEKLOKSIISTFGF 791	
QY	94 NESLVDYNSVL-----INERDEKGNFVELGAPFLLESNAHFNL--PVNTSISVVQ 144	
DB	792 TNDLGSFLQVVKSKSLSSVEQDKFTSSLKEVSVFVKSENKVLSSAGTYLSNIE 851	
QY	145 LPTNVYKDPDILNGVYSEALNAVVENFQDPTL-----TWQYFGSATGFERI 194	
DB	852 L-----FKNSDVPKGFPS-----HILNFKETPELLNKIIDYVINSWESIDQYNDAPEF 900	
QY	195 YPGIKWTPDENGVTTCRNRGWYIQAAATSPKDI---VILVDVS-----GSMK 239	
DB	901 -----VLNFKLTSSWF---KTVVKDIFSSVNVSEIQYANILTSKLKLSQA 945	
QY	240 GLRMT-----TA-KHTITILD-----TLGENDFVNIIAYNDVHYI 275	

DB	946 GFELTNSSVESIKNIETNTLKIIADNNTIDALVDFTFVNSKTLLEIDKKNPFA----- 997	
QY	276 EPCFKGILVQADRDNR--BHFKLLVBEELMVKGVGVVDQALREAFQILKQ--FOEAKQGS 331	
DB	998 --SLKNIQIFALSDDNPFVFKALISSNKKOKAFVNYQKQDITNVLKELLPE----- 1049	
QY	332 CNOAIMLISDGAVEDYEPVFEKYNWPDCKRVFTYILIGR-----EVSFADRMKWIACNNK 386	
DB	1050 --KFFNLIIYSFMPKPTSELF--NNPEALNKTTTILRNALKKQLDPDFINKMDIIFDNL 1105	
QY	387 GYVTOIST-----LADTQENVMYHLVLSRPVNHHD-HDI1-----WTEAYWDSK 431	
DB	1106 DKYQKULENTGVGLILKDNDSOAIATKQVAFKDVVNEANFQDVLKVLVLSQTKFMGFE 1165	
QY	432 LLSQAQSL-TLITTVAMPVFSKKNETRSHGILLGVVGSVALRELMLKAPRYKLGVHG 490	
DB	1166 LNADETINKISTDLTKILKQVFESNNFAKS-----LALATKDSLVIDGV 1208	
QY	491 -----AFLNTWNGYILSHPDRLRPLYREGKUKPKPNYSV-----DLSVEVEDQA 536	
DB	1209 QANKKIFDPTFRPLNT---FLLSEK-----EKTKENYQMKVKSILNTKLIDISQNS 1255	
QY	537 ESLRTAMINRETCTLSMD-----VKVPMDKGRVLFITNDYFF-----TDISD- 579	
DB	1256 ESINKLLKTTKSAUSLRDEFEYKTIKVFUSKEKLASAYTPVVEFVKVLKNEKTTNFSDL 1315	
QY	580 -----TPFS-----LGAVLS- 589	
DB	1316 LIDSLFKDFSQQAQNSFELIYLVLRNNKETVNVYLKELSPFIKSSNIIQRLLGQTINA 1375	
QY	590 --RGHGEYI-----LLGNTSVBEGLDHLLHPDLALAGDWIYCYTDD 629	
DB	1376 LVTPNGEKIFSDTELQSLSTLINESLDLFGKTNIIISNLDYLVLSALSINQESSVLTKVE 1435	
QY	630 P-DHRKLSQLE---AMIR-FLTRKDPDLSCDBELVREVLFDVV 668	
DB	1436 NITHKALDQONSFYFAVIKTLTLLSVKEGVDKSDS-----FKAI 1473	

Search completed: November 16, 2005, 03:24:34
Job time : 54 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2005, 03:12:42 ; Search time 188 Seconds
(without alignments)
2968.970 Million cell updates/sec

Title: US-09-833-222a-10
Perfect score: 5726
Sequence: 1 MAVALGTRRRDRVKLWADTF.....MPNMTVPVLLGGNIRVYAL 1090

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5399.5	94.3	1120	Q81ZS9	Q81ZS9 homo sapien
2	5373.5	93.8	1137	Q7Z3S7	Q7Z3S7 homo sapien
3	4649	81.2	974	Q7Z3S8	Q7Z3S8 homo sapien
4	3422	59.8	1091	Q9Z1L5	Q9Z1L5 mus musculus
5	3416.5	59.7	1091	Q81ZS8	Q81ZS8 homo sapien
6	3410	59.6	1085	Q8CFG5	Q8CFG5 rattus norv
7	3250.5	56.8	997	Q9NY16	Q9NY16 homo sapien
8	1866.5	32.6	519	Q9NY18	Q9NY18 homo sapien
9	1551	27.1	1218	Q9V6T7	Q9V6T7 drosophila
10	1496.5	26.1	1170	Q81P22	Q81P22 drosophila
11	1441	25.2	2190	Q9VJM0	Q9VJM0 drosophila
12	1430.5	25.0	1028	Q7Q758	Q7Q758 anopheles g
13	1398	24.4	1011	Q7PM00	Q7PM00 anopheles g
14	1305.5	22.8	1255	Q9NK83	Q9NK83 drosophila
15	1283	22.4	1120	Q9VJN7	Q9VJN7 drosophila
16	1262	22.0	394	Q8AVV7	Q8AVV7 xenopus lae
17	1243	21.7	967	Q7PM11	Q7PM11 anopheles g
18	1189	20.8	1098	Q8CHE9	Q8CHE9 mus musculus
19	1183.5	20.7	1076	Q9U5W0	Q9U5W0 homo sapien
20	1183.5	20.7	1145	Q9Y268	Q9Y268 homo sapien
21	1182.5	20.7	1157	Q8CFG6	Q8CFG6 rattus norv
22	1182	20.6	1084	Q9Z0H6	Q9Z0H6 mus musculus
23	1182	20.6	1156	Q9EQG2	Q9EQG2 mus musculus
24	1180	20.6	1148	Q8C8R8	Q8C8R8 mus musculus
25	1174.5	20.5	1143	Q9NY48	Q9NY48 homo sapien
26	1173	20.5	1154	Q6PHS9	Q6PHS9 mus musculus
27	1171.5	20.5	1186	Q6REE3	Q6REE3 mus musculus
28	1171	20.5	1150	Q9NY47	Q9NY47 homo sapien
29	1109	19.4	1084	Q8CFG7	Q8CFG7 rattus norv
30	1106.5	19.3	1103	C1C2 MOUSE	Q08532 mus musculus
31	1105.5	19.3	1091	Q9ER53	Q9ER53 rattus norv

ALIGNMENTS

RESULT 1

ID	Q81ZS9	PRELIMINARY;	PRT;	1120 AA.
AC	Q81ZS9;			
DT	01-MAR-2003 (TrEMBLrel. 23, Created)			
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
DE	Voltage-gated calcium channel alpha (2)delta-4 subunit.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=22169250; PubMed=12181424;			
RA	Qin N., Yagel S., Mompalao M.L., Codd E.E., D'Andrea M.R.;			
RT	"Molecular cloning and characterization of the human voltage-gated			
RT	calcium channel alpha (2)delta-4 subunit."			
RL	Mol. Pharmacol. 62:485-496(2002).			
DR	EMBL; AF516695; AAN06672.1; -			
DR	GO; GO:0016020; C:membrane; IEA.			
DR	InterPro; IPR004010; Cache.			
DR	InterPro; IPR002035; VWF_A.			
DR	Pfam; PF02743; Cache; 2.			
DR	Pfam; PF00092; VWA; 1.			
DR	SMART; SM00327; VWA; 1.			
DR	PROSITE; PS0234; VWEA; 1.			
SQ	SEQUENCE 1120 AA; 126204 MW; 4F950C11C3249984 CRC64;			
Query Match 94.3%; Score 5399.5; DB 2; Length 1120;				
Best Local Similarity 98.2%; Pred. No. 0;				
Matches 1035; Conservative 5; Mismatches 11; Indels 3; Gaps 2;				
QY	11	DRVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESLSLKEEVDGLVLRKFKFEDMENML	70	
Db	58	ETVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESLSLKEEVDGLVLRKFKFEDMENML	117	
QY	71	RRKVEAVQNVLVEAAEADLNHEFNESLSVFDYNSVLINERDEKGNFVGLGAELLESNAH	130	
Db	118	RRKVEAVQNVLVEAAEADLNHEFNESLSVFDYNSVLINERDEKGNFVGLGAELLESNAH	177	
QY	131	FSNLPNTSISSVQLPTNTYNTKDPDILNGVYNSALNAVFNFORPDTLTWQYFGSATG	190	
Db	178	FSNLPNTSISSVQLPTNTYNTKDPDILNGVYNSALNAVFNFORPDTLTWQYFGSATG	237	
QY	191	FRFRIYIGIKWTDPDENGVIITFDCNRNRMVYQAATSPKDIIVLVDVSGSMKGLRMTIAKHTI	250	
Db	238	FRFRIYIGIKWTDPDENGVIITFDCNRNRMVYQAATSPKDIIVLVDVSGSMKGLRMTIAKHTI	297	
QY	251	TTILDTLGENDFWIIAYNDYVHYIEPCPKGILVQADRNREHFLLVEELMVGKGVVD	310	
Db	298	TTILDTLGENDFWIIAYNDYVHYIEPCPKGILVQADRNREHFLLVEELMVGKGVVD	357	
QY	311	QALREAFQILKQFEAKQCSLNCQA1MLISDGAVEDYEPVFEXYNWPCDKRVFTYLIGR	370	

Q8VHS9 rattus norv
Q77773 sus scrofa
Q72621 homo sapien
P13806 oryctolagus
Q9UIU0 homo sapien
P54289 homo sapien
P54290 rattus norv
Q86XZ5 homo sapien
Q9SR75 drosophila
P34374 caenorhabdi
Q9UDQ3 homo sapien
Q17517 caenorhabdi
Q7JMF9 caenorhabdi
Q8JFR4 brachydanio

Db 358 QALREAFQILKQFOEAQSGSLCNOAIIMLISDGAVEDYEPVFEKYNWPCDKRVFTYLIGR 417
Qy 371 EVSPADRMKIACNNKGYTQISTLATQENVMYHLVSRPMVINHDHDIWTEAYMDS 430
Db 418 EVSPADRMKIACNNKGYTQISTLATQENVMYHLVSRPMVINHDHDIWTEAYMDS 477
Qy 431 KLLSSQAQSLTLTTVAMPVFSKKNETRSKNGILLGVVGSVALRELKMLAPRYKLGHVGY 490
Db 478 KLLSSQAQSLTLTTVAMPVFSKKNETRSKNGILLGVVGSVALRELKMLAPRYKLGHVGY 537
Qy 491 AFLNTNNGYILSHPDRLPLRYREGKLLKPKPNYNSVDLSEVEWDOAESLRTAMINRETGT 550
Db 538 AFLNTNNGYILSHPDRLPLRYREGKLLKPKPNYNSVDLSEVEWDOAESLRTAMINRETGT 597
Qy 551 LSMGVKVPMDKGRVLFNTDYFTDIDSDTFFSLGAVLSRGHGEYILLGNNTSVEEGLHDL 610
Db 598 LSMGVKVPMDKGRVLFNTDYFTDIDSDTFFSLGAVLSRGHGEYILLGNNTSVEEGLHDL 657
Qy 611 LHPDLALAGDWIYICITDIDPDHRLKLSOLEAMIRFLTRKDPDLECEBELVREVLFDVAVTA 670
Db 658 LHPDLALAGDWIYICITDIDPDHRLKLSOLEAMIRFLTRKDPDLECEBELVREVLFDVAVTA 717
Qy 671 PMEAYWTALALNNSESEHVVDMFLGTRAGLLRSSLFGVSEKVSQRKFLTPDEASVFT 730
Db 718 PMEAYWTALALNNSESEHVVDMFLGTRAGLLRSSLFGVSEKVSQRKFLTPDEASVFT 777
Qy 731 LDRFPPLYRQASEHPAGSFVFNLRWAGPESAGEPMVVTASTAVAVTVDKRTAIAAAGV 790
Db 778 LDRFPPLYRQASEHPAGSFVFNLRWAGPESAGEPMVVTASTAVAVTVDKRTAIAAAGV 837
Qy 791 QMKLEFLQRFKWAATRCQSTVDGPYTQSCDSLDLCEVDINNGFILLISKRSTGRFLGE 850
Db 838 QMKLEFLQRFKWAATRCQSTVDGPYTQSCDSLDLCEVDINNGFILLISKRSTGRFLGE 897
Qy 851 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHSAAQPLVSPISAFPLATRWLLQELVL 910
Db 898 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHSAAQPLVSPISAFPLATRWLLQELVL 957
Qy 911 FLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLOPCDTEYPVFPVQPAIREANGIVECG 970
Db 958 FLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLOPCDTEYPVFPVQPAIREANGIVECG 1017
Qy 971 PCQKVFVVOQIPNSNLLLVTDPTCDCSIIPPVLQATEVKYNASVKCDRMRSQKLRRRP 1030
Db 1018 PCQKVFVVOQIPNSNLLLVTDPTCDCSIIPPVLQATEVKYNASVKCDRMRSQKLRRRP 1077
Qy 1031 DSCHAFHPVREADRAGWAGFSNP--LCLGLC 1062
Db 1078 DSCHAFHPREENAQ-DCGGASDTGASPLLLLPVC 1110

RESULT 2

Q723S7
ID Q723S7 PRELIMINARY; PRT; 1137 AA.
AC Q723S7;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Hypothetical protein DKF2p686O0495.
GN Name=DKF2p686O0495;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa;
OC Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human retina;
RA Bloembergen H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX537437; CAD97679.1; -;
GO; GO:0016020; C:membrane; IEA.

DR InterPro: IPR004010; Cache.
DR InterPro: IPR002035; VWF_A.
DR Pfam: PF02743; Cache; 2.
DR Pfam: PF00092; VWA; 1.
DR SMART: SM00327; VWA; 1.
DR PROSITE: PS0234; VWFA; 1.
KW Hypothetical protein.
SQ SEQUENCE 1137 AA; 127965 MW; 69410B72580F3FF7 CRC64;

Query Match 93.8%; Score 5373.5; DB 2; Length 1137;
Best Local Similarity 97.8%; Pred. No. 1.6e-317;
Matches 1031; Conservative 5; Mismatches 15; Indels 3; Gaps 2;

Qy 11 DRVKLWADTFGGDLVNTVTKYSGSLLLQKKYKDVSSSLKTEIEVDGLVSRKFSDEMNML 70
Db 75 ETVKLWADTFGGDLVNTVTKYSGSLLLQKKYKDVSSSLKTEIEVDGLVSRKFSDEMNML 134
Qy 71 RRKVEAVQNLEAAEADLNHEFNESLVFDYNSVLINERDEKGNFVELGAEFLLESNAH 130
Db 135 RRKVEAVQNLEAAEADLNHEFNESLVFDYNSVLINERDEKGNFVELGAEFLLESNAH 194
Qy 131 FSNLPVNTSISSVQLPTNVYTKDPDILNGVYMSALNAVVENFQRPDPLTWYQFSGATG 190
Db 195 FSNLPVNTSISSVQLPTNVYTKDPDILNGVYASEALNAVVENFQRPDPLTWYQFSGATG 254
Qy 191 FRRIYPGIKWTPDENGVITFDCNRNGWYIOAATSPKDIIVLDVSGSMKGLRMTIAKHITI 250
Db 255 FRRIYPGIKWTPDENGVITFDCNRNGWYIOAATSPKDIIVLDVSGSMKGLRMTIAKHITI 314
Qy 251 TTILDTLGENDFVNIITAYNDYVHYIEPCFKGILVQADRDNRHFKLLVEELMVKGVGVND 310
Db 315 TTILDTLGENDFVNIITAYNDYVHYIEPCFKGILVQADRDNRHFKLLVEELMVKGVGVND 374
Qy 311 QALREAFQILKQFOEAQSGSLCNOAIIMLISDGAVEDYEPVFEKYNWPCDKRVFTYLIGR 370
Db 375 QALREAFQILKQFOEAQSGSLCNOAIIMLISDGAVEDYEPVFEKYNWPCDKRVFTYLIGR 434
Qy 371 EYSPADRMKIACNNKGYTQISTLATQENVMYHLVSRPMVINHDHDIWTEAYMDS 430
Db 435 EYSPADRMKIACNNKGYTQISTLATQENVMYHLVSRPMVINHDHDIWTEAYMDS 494
Qy 431 KLLSSQAQSLTLTTVAMPVFSKKNETRSKNGILLGVVGSVALRELKMLAPRYKLGHVGY 490
Db 495 KLLSSQAQSLTLTTVAMPVFSKKNETRSKNGILLGVVGSVALRELKMLAPRYKLGHVGY 554
Qy 491 AFLNTNNGYILSHPDRLPLRYREGKLLKPKPNYNSVDLSEVEWDOAESLRTAMINRETGT 550
Db 555 AFLNTNNGYILSHPDRLPLRYREGKLLKPKPNYNSVDLSEVEWDOAESLRTAMINRETGT 614
Qy 551 LSMGVKVPMDKGRVLFNTDYFTDIDSDTFFSLGAVLSRGHGEYILLGNNTSVEEGLHDL 610
Db 615 LSMGVKVPMDKGRVLFNTDYFTDIDSDTFFSLGAVLSRGHGEYILLGNNTSVEEGLHDL 674
Qy 611 LHPDLALAGDWIYICITDIDPDHRLKLSOLEAMIRFLTRKDPDLECEBELVREVLFDVAVTA 670
Db 675 LHPDLALAGDWIYICITDIDPDHRLKLSOLEAMIRFLTRKDPDLECEBELVREVLFDVAVTA 734
Qy 671 PMEAYWTALALNNSESEHVVDMFLGTRAGLLRSSLFGVSEKVSQRKFLTPDEASVFT 730
Db 735 PMEAYWTALALNNSESEHVVDMFLGTRAGLLRSSLFGVSEKVSQRKFLTPDEASVFT 794
Qy 731 LDRFPPLYRQASEHPAGSFVFNLRWAGPESAGEPMVVTASTAVAVTVDKRTAIAAAGV 790
Db 795 LDRFPPLYRQASEHPAGSFVFNLRWAGPESAGEPMVVTASTAVAVTVDKRTAIAAAGV 854
Qy 791 QMKLEFLQRFKWAATRCQSTVDGPYTQSCDSLDLCEVDINNGFILLISKRSTGRFLGE 850
Db 855 QMKLEFLQRFKWAATRCQSTVDGPYTQSCDSLDLCEVDINNGFILLISKRSTGRFLGE 914
Qy 851 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHSAAQPLVSPISAFPLATRWLLQELVL 910
Db 915 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHSAAQPLVSPISAFPLATRWLLQELVL 974

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Qy 911 FLEWSVWGSDYDRGAEAKSVFHHSHKHKQDPLQPCDTEVPVYQPAIREANGIVECG 970
Db 975 FLEWSVWGSDYDRGAEAKSVFHHSHKHKQDPLQPCDTEVPVYQPAIREANGIVECE 1034
Qy 971 PCQKVFVVOQIPNSNLVLLVTDPTCDSCIFPPVLOEATEVKYNASVKCDRMRSKLRRRP 1030
Db 1035 PCQKVFVVOQIPNSNLVLLVTDPTCDSCIFPPVLOEATEVKYNASVKCDRMRSKLRRRP 1094
Qy 1031 DSCAFHPEVRVEADRGWAGFSNP--LCIGLC 1062
Db 1095 DSCAFHPEVNAQ--DCGASDTSAPPLLLPVC 1127

RESULT 3
Q723S8
ID Q723S8 PRELIMINARY; PRT; 974 AA.
AC Q723S8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Hypothetical protein DRF2p686A1395.
GN Name=DKF2p686A1395;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human retina;
RA Bloecher H., Boscher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX537436; CAD97678.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF02743; Cache; 2.
DR SMART; SM00092; VWA; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS50234; VWFA; 1.
KW Hypothetical protein.
SQ
SEQUENCE 974 AA; 109568 MW; 6F3C91CD0A038ED2 CRC64;

Query Match 81.2%; Score 4649; DB 2; Length 974;
Best Local Similarity 99.4%; Pred. No. 1.3e-273;
Matches 895; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 11 DRVKLWADTFGGDLYNTVTKYSGSLQLQKKYKDVESLKIIEVDGLVLRKFSDEMNL 70
Db 75 ETVKLWADTFGGDLYNTVTKYSGSLQLQKKYKDVESLKIIEVDGLVLRKFSDEMNL 134

Qy 71 RRYEAVQNLVEAAEEADLNHEPNESLVFDYNSVLINERDEKGNFVELGAEPFLLENAH 130
Db 135 RRYEAVQNLVEAAEEADLNHEPNESLVFDYNSVLINERDEKGNFVELGAEPFLLENAH 194

Qy 131 FSNLPVNTSISGVLPNTVYNKOPDILNGVYMSALNAVVFENFQRPDPTLWYFGSATG 190
Db 195 FSNLPVNTSISGVLPNTVYNKOPDILNGVYMSALNAVVFENFQRPDPTLWYFGSATG 254

Qy 191 FFRIYPGIKWTPDNGVITFCRNRGVYQAATSPKQIVLVVDVSGSMKGLRMTIAKHTI 250
Db 255 FFRIYPGIKWTPDNGVITFCRNRGVYQAATSPKQIVLVVDVSGSMKGLRMTIAKHTI 314

Qy 251 TTILDTLGENDFVNIIVNDVHYIEPCFKGILVQADRNRHFKLLVEELMWKGVGVVD 310
Db 315 TTILDTLGENDFVNIIVNDVHYIEPCFKGILVQADRNRHFKLLVEELMWKGVGVVD 374

Qy 311 QALREAFQILKQFEAKQGSGLCNQAIMLISDGAVEDYEPVEKYNWPDCKVRVFTYLIGR 370
Db 375 QALREAFQILKQFEAKQGSGLCNQAIMLISDGAVEDYEPVEKYNWPDCKVRVFTYLIGR 434

Qy 371 EVSFADRMKVIACNNKGYTQISTLATQENVMYHLVLSRPMVINHDHDIITWEAYMDS 430

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Db 435 EVSFADRMKVIACNNKGYTQISTLATQENVMYHLVLSRPMVINHDHDIITWEAYMDS 494
Qy 431 KLASQAQSLTLLTTVAMPVFSKKNETRSRSHGILLGVVGSVDVALRELKMLAPRYKLGVRHG 490
Db 495 KLASQAQSLTLLTTVAMPVFSKKNETRSRSHGILLGVVGSVDVALRELKMLAPRYKLGVRHG 554
Qy 491 AFLNTNNGYILSHPDPLRPLREGKKLKPKNYNSVDLSEVWEDQAESLRTAMINRETGT 550
Db 555 AFLNTNNGYILSHPDPLRPLREGKKLKPKNYNSVDLSEVWEDQAESLRTAMINRETGT 614
Qy 551 LSHMDVKVPMDKGRKRVLFNTDYFFTDISDTPFSLGAVLSRGHGYYILLGNTSVBEGLDL 610
Db 615 LSHMDVKVPMDKGRKRVLFNTDYFFTDISDTPFSLGAVLSRGHGYYILLGNTSVBEGLDL 674
Qy 611 LHPDLALAGDWIYCITDIDPDHRLKLSQLEAMIRELTRKDPDLECEELVREVLFDVVTA 670
Db 675 LHPDLALAGDWIYCITDIDPDHRLKLSQLEAMIRELTRKDPDLECEELVREVLFDVVTA 734
Qy 671 PMEAYWTALALNMSESESEHVVDMAFITRAGLLRSSLFGVSEKYSDDRFLTPEDASVFT 730
Db 735 PMEAYWTALALNMSESESEHVVDMAFITRAGLLRSSLFGVSEKYSDDRFLTPEDASVFT 794
Qy 731 LDRPPLVYRQASEHPAGSFVFNLRWAGSPESAGSPMVVVTASTAVAVTVDKRTATAAAAGV 790
Db 795 LDRPPLVYRQASEHPAGSFVFNLRWAGSPESAGSPMVVVTASTAVAVTVDKRTATAAAAGV 854
Qy 791 QMKLEFLQRFWAATROCSITVDGPTQSCEDSDLDLCFVIDNNGFILISKRSRGTGRFLGE 850
Db 855 QMKLEFLQRFWAATROCSITVDGPTQSCEDSDLDLCFVIDNNGFILISKRSRGTGRFLGE 914
Qy 851 VDGAVALTQLLSMGVFSQVMTDYQAMCKPSHHSHHSAQPLVSPISAFJATATRWLLQELVL 910
Db 915 VDGAVALTQLLSMGVFSQVMTDYQAMCKPSHHSHHSAQPLVSPISAFJATATRWLLQELVL 974

RESULT 4
Q9Z1L5
ID Q9Z1L5 PRELIMINARY; PRT; 1091 AA.
AC Q9Z1L5;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Calcium channel alpha-2-delta-C subunit.
GN Name=Cacna2d3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Klugbauer N., Lacinova L., Marais E., Hobom M., Hofmann F.;
RT "Molecular diversity of the calcium channel alpha2delta subunit.";
RL J. Neurosci. 19:648-691(1999).
DR EMBL; AJ010949; CAA09423.1; -.
DR PIR; T30256; T30256.
DR MG; MG:1338890; Cacna2d3.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF02743; Cache; 2.
DR Pfam; PF00092; VWA; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS50234; VWFA; 1.
SQ
SEQUENCE 1091 AA; 122777 MW; 7AEE2BDA10077A0A CRC64;

Query Match 59.8%; Score 3422; DB 2; Length 1091;
Best Local Similarity 60.0%; Pred. No. 5.5e-199;
Matches 627; Conservative 188; Mismatches 212; Indels 18; Gaps 6;

Qy 13 VKLWADTFGGDLYNTVTKYSGSLQLQKKYKDVESLKIIEVDGLVLRKFSDEMNL 72
Db 42 VKLWASAFGGEIKSIAAKYSGSLQLQKKYKDVESLKIIEVDGLVLRKFSDEMNL 101

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QY 73 KVEAVQNLVEAABEADLNHEFNESLVFDYNSVLINERDEKGNFVGLGABFLLESNAHFS 132
DB 102 KSEAVRRLVEAABEAEHLKHEFDADLQYEFNAVLINERDKGNFLEGLKGFILAPNDHFN 161
QY 133 NLPVNTSISSVOLPTNVYKDPDILNGVYMSALNAVFNFORPDLTWQYFGSATGFF 192
DB 162 NLPVNISLSDVQVPTNMYNKDPAIVNGVYMSLKNVFNDFDRDPSLIWQYFGSAKGF 221
QY 193 RIYPGIKWTPDENGVIITFCRNRGWYIQAATSPKDIIVLDVSGSMKGLRTAKHTITT 252
DB 222 ROYPGIKWEPDENGVIATFCRNRKWIQAATSPKDVVILVDVSGSMKGLRTIAKTQVSS 281
QY 253 ILDTLGENDFVNIITAYNDVYHYIIBPCFKILVQADRNREHFKLLVBEELMVKGVVVDQA 312
DB 282 ILDTLGDDDFNIIITAYNEELHYVEPCLNGTLVQADRTNKEHFRHLDKLFAKIGMLDIA 341
QY 313 LREAFQILKQFQEAQKQSLCNQAIIMLISDGAVEDYEPVPEKYNPDCKVRVFTYLIQREV 372
DB 342 LNEAFNLSDFNHTGOGSICSAQIMLITDGAVDYDTIFAKYNWPDVKRVIIFTYLIQREA 401
QY 373 SFADRMKWIACNNKGYTQISTLADTQENMVEYLHVLSPMVTNHDDIITWEAYMDSKL 432
DB 402 AFADNLKMACANKGFTQISTLADVQENMVEYLHVLSPKVIDQEHVVWTEAYIDSTL 461
QY 433 LSSQA-----QSLTLLTTVAMPVFSKNETRSHGILLGVGSDVALRELKMLAPRYKLGVH 488
DB 462 POAKLADDDQGLVMTTAVMPVFSKNETRSHGILLGVGSDVLPVKELLXTIPKYLGIH 521
QY 489 GYAFALNTNGVYILSHPDRLPLREGKLLKPKPNVNSVDLSEVEDOQESLRTAMINRET 548
DB 522 GYAFATNNGVYILTHPELRLLYEEGKK-RRKPNYSVDLSEVEDWDRDDVLRLNVMNRKT 580
QY 549 GTLSMDVKVPMDKGRVLFNTDYYFTDI SDTPFSLGAVLSRGHGEVILLGNTSVBGLH 608
DB 581 GKFSMEVKKTVDKGRVLMVNTDYYTIDIKGTPSLGVALSRGHGKYFFRGNTYIEBGLH 640
QY 609 DLLHPLDALAGDWTYCTIDDPHRLKLSQLEAMIRFLTRKDPDLECDLVEELVRELVFVAV 668
DB 641 DLEHPDVSADSESYCNTDLHPEHRHLSQLEAIKLYLKGKPELLOCDKELIQEVLFDVAV 700
QY 669 TAPWEAWTALANMSESHVDMAPLGTAGLLRSSLFVSGSEKVSDRKFLTPEDASV 728
DB 701 SAPIEAWTSLANKSENSDKGEVAPLGTGLSLINLFPVGAELTNODFLKAGDKENI 760
QY 729 FTLDRLPLWYRQASEHPAGSFVFNLRWAEPSGEPMVVTTASTAVAVTDKETAIAAAA 788
DB 761 FNADHFLWYRRAEQTAGSFVYSIPFSTG--TVNKSNNVVTASTSLOLDERKSPVVAAV 818
QY 789 GVQMKLEFLQRFKWAATROGSTVDGPYTQSCEDSDLDCTFVIDNNGFTILISKRSRETGRFL 848
DB 819 GIQMKLEFFQRFKWTASROCASLDGKCSISODDETVCNYLIDNNGFLVSEDTYTGDF 878
QY 849 GEVDGAVLTOLLNGVFSQVMTDYQAMCKPSSHHSAAQPLVSPISAFITATRWLLQEL 908
DB 879 GEVEGAVNNKLLTWGSPKRTLYDYQAMCRANKESSDSAGHLDPYKAFLSAAKWIMTEL 938
QY 909 VLFLELVSVMGSDVRCAGAEAKSVFHHSHKHQDPLQPCDTEYPVFVYQPAIBEANGIVE 968
DB 939 VLFLEVFNLCS-SWHSMTAKA-----QKLQTLPEPCDTEYPAFVSEKTIKETTGNIA 990
QY 969 CGPQKQVYVQIQPNLSNLLLVTDPTCDCTCISFFPVQLQEAETKYNASVKCDRMSQKLRR 1028
DB 991 CEDCSKSFVLIQIPSSNLFVWVDSCLCESVAPITWAPIETIYRNSLKCERLKAQKIRR 1050
QY 1029 RPDSCHAHPHEVRVADRGRWAGFSS 1053
DB 1051 RPSCSGFHPHPE---ENARECGGASS 1072

RESULT 5
Q81ZS8 PRELIMINARY; PRT; 1091 AA.
ID Q81ZS8

Q81ZS8;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Voltage-gated calcium channel alpha (2)delta-3 subunit.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22169250; PubMed=12181424;
RA Qin N., Yagel S., Moplaisir M.L., Codd E.E., D'Andrea M.R.;
RT "Molecular cloning and characterization of the human voltage-gated
calcium channel alpha(2)delta-4 subunit.";
RL Mol. Pharmacol. 62:485-496(2002).
DR EMBL; AF516696; AAN06673.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF02743; Cache; 2.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS0234; VWFA; 1.
SQ SEQUENCE 1091 AA; 123010 MW; 4E5E0BD38F05082 CRC64;

Query Match 59.7%; Score 3416.5; DB 2; Length 1091;
Best Local Similarity 60.3%; Pred. No. 1.2e-198;
Matches 623; Conservative 188; Mismatches 203; Indels 19; Gaps 6;

QY 13 VKLWADTFGGDLNTVTYKSYGSLLLQKKYKDVESLKIIEVDGLVRFKSEMMNLR 72
DB 42 VKLWASAFGEIKSIAAKYSGSLLQKKYKEYEKDVAIBEIDGLQVLKAKNMEFHK 101
QY 73 KVEAVQNLVEAABEADLNHEFNESLVFDYNSVLINERDEKGNFVGLGABFLLESNAHFS 132
DB 102 KSEAVRRLVEAABEAEHLKHEFDADLQYEFNAVLINERDKGNFLEGLKGFILAPNDHFN 161
QY 133 NLPVNTSISSVOLPTNVYKDPDILNGVYMSALNAVFNFORPDLTWQYFGSATGFF 192
DB 162 NLPVNISLSDVQVPTNMYNKDPAIVNGVYMSLKNVFNDFDRDPSLIWQYFGSAKGF 221
QY 193 RIYPGIKWTPDENGVIITFCRNRGWYIQAATSPKDIIVLDVSGSMKGLRTAKHTITT 252
DB 222 ROYPGIKWEPDENGVIATFCRNRKWIQAATSPKDVVILVDVSGSMKGLRTIAKTQVSS 281
QY 253 ILDTLGENDFVNIITAYNDVYHYIIBPCFKILVQADRNREHFKLLVBEELMVKGVVVDQA 312
DB 282 ILDTLGDDDFNIIITAYNEELHYVEPCLNGTLVQADRTNKEHFRHLDKLFAKIGMLDIA 341
QY 313 LREAFQILKQFQEAQKQSLCNQAIIMLISDGAVEDYEPVPEKYNPDCKVRVFTYLIQREV 372
DB 342 LNEAFNLSDFNHTGOGSICSAQIMLITDGAVDYDTIFAKYNWPDVKRVIIFTYLIQREA 401
QY 373 SFADRMKWIACNNKGYTQISTLADTQENMVEYLHVLSPMVTNHDDIITWEAYMDSKL 432
DB 402 AFADNLKMACANKGFTQISTLADVQENMVEYLHVLSPKVIDQEHVVWTEAYIDSTL 461
QY 433 LSSQAQSLT-----LLTTVAMPVFSKNETRSHGILLGVGSDVALRELKMLAPRYKL 486
DB 462 --PQAQKLTDDQGPVLMTTVAMPVFSKNETRSHGILLGVGSDVLPVKELLKTIPYKL 519
QY 487 VHGYAFALNTNGVYILSHPDRLPLREGKLLKPKPNVNSVDLSEVEDOQESLRTAMINR 546
DB 520 IHGYAFATNNGVYILTHPELRLLYEEGKK-RRKPNYSVDLSEVEDWDRDDVLRLNVMNR 578
QY 547 ETGTLSDMDVKVPMDKGRVLFNTDYYFTDI SDTPFSLGAVLSRGHGEVILLGNTSVBGL 606
DB 579 KTGKFSMEVKKTVDKGRVLMVNTDYYTIDIKGTPFSLGVALSRGHGKYFFRGNTYIEB 638
QY 607 LHDLLHPLDALAGDWTYCTIDDPHRLKLSQLEAMIRFLTRKDPDLECDLVEELVRELVF 666
DB 639 LHDLEHPDVSADSESYCNTDLHPEHRHLSQLEAIKLYLKGKPELLOCDKELIQEVLFD 698

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Qy 667 VVTAPMEAYTALALNMSBESEHVVDMAFLCTRAGLLRSSLFVSGSEKVSDDRKFLTPEDBA 726
Db ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
699 VVSAPIEAYMTSLALNKSNSDKGEVAFGLTRTGLSLRNLFVGAEOQLTNQDFLKAGDK 758
Qy 727 SVFTLDPEPLWYROASEHPAGSFVFNLRWAGSPESAGEPMVVTASTAVAVTVDKRTAIA 786
Db ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
759 NIFNADHPFLWYRAAEIOIGSFVSIPTSTGP--VNKSNVVTASTSIQLLDERKSPVVA 816
Qy 787 AAGVQMKLEFQRFKFWAATROCSVDGPTQSCDSLDLDFVINDNNGFILISKESRETGR 846
Db ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
817 AVGLQMKLEFQRFKFWAATROCSVDGPTQSCDSLDLDFVINDNNGFILISKESRETGR 876
Qy 847 FLGEVQAVLTQLLSMGVFSVOTWYDQAMCKPSSHHSAAOPLVSPISAFLTATRLMLLQ 906
Db ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
877 PFGIEGAVNMKLLTMSGSKRITLYDQAMCRANKESDGAHGLLDYPNAPLSAVKIMT 936
Qy 907 ELVLFLLEWSVMSWYDGAERAKSFVHSHKHKKQDPLQPCDTEYVPVYQPAIREANGI 966
Db ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
937 ELVLFLVEFNLC-SWVHSDMTAKA-----OKLKQTLPECDTEYPAFVSERTIKETGN 988
Qy 967 VECGPGCKVFVVOQIPNSNLLLVTDPTDCSIFPPVLQEADEVKNASVKCDMRMSOKL 1026
Db ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
989 IACEDCKSFVIOIPNSNLFVVDSSCLCESVAPITMAPIBIRYNESLKCERLKAQKI 1048
Qy 1027 RRRPDSCHAFHPE 1039
Db ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
1049 RRRPESCHGFHPE 1061

RESULT 6
Q8CFG5
ID AC Q8CFG5 PRELIMINARY; PRT; 1085 AA.
RC STRAIN=Sprague-Dawley; TISSUE=atrium;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Calcium channel alpha-2 delta-3 subunit.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=atrium;
RA Chu P.-J., Best P.M.;
RL Submitted (FBI-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF486278; AA014654.1;
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR04010; Cache.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF02743; Cache; 2.
DR Pfam; PF00092; VWA; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS0234; VVFA; 1.
SQ SEQUENCE 1085 AA; 122203 MW; 9584F533E18002A CRC64;

Query Match 59.6%; Score 3410; DB 2; Length 1085;
Best Local Similarity 59.8%; Pred. No. 2.9e-198;
Matches 622; Conservative 191; Mismatches 212; Indels 16; Gaps 6;

Qy 13 VKLWADTFGGDLVNTVTKYSGLLQKKYKDVSSSLKIEEVDGLVKRFSEDMENLRR 72
Db ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
42 VKLWASAFGGGEIKAIKYSQSLQKKYKEYEKDVAIEIDGLQLVKLAKWNEEFHK 101

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Qy 73 KVEAVQNLVRAAEADLNHEFNESLVDYVNSVLINERDEKGNFVGLGABFLLESNAHFS 132
Db ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
102 KSEAVRELVAABEAHLKHFBDADLQYEVNAVILINERDKDGNFLGKPEFILAPNDHFN 161
Qy 133 NLPVNTSISSVOLPTNVYNDPDLNLGVMSALNAVVENFORDPTLTWQYFSGSATGFF 192
Db ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
162 NLPVNTSISSVOLPTNVYNDPDLNLGVMSALNAVVENFORDPTLTWQYFSGSATGFF 221
Qy 193 RIYPGIKWTDPENGVIITFCRNRGWYIOAATSPKDIIVLDVDSGSMKGLRMTIAKHITT 252
Db ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
222 ROYPGIKWEPDENGVIITFCRNRGWYIOAATSPKDIIVLDVDSGSMKGLRMTIAKHITT 281
Qy 253 ILDTLGENDFNIIAYNDYHYIYPCFKGILVQADNRNREHFKLLVBEMLVGVGVDDQA 312
Db ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
282 ILDTLGDGDFNIIAYNDYHYIYPCFKGILVQADNRNREHFKLLVBEMLVGVGVDDQA 341
Qy 313 LRBAFOILKFOBAKQSGSLCNOALMLISDGAVEDYEPVEKYNWPCDKRVFTVYLIGREV 372
Db ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
342 LNEAFNVLSDFNHTGQSGISQALMLITDGAVDYDIFAKYNWPERKVRIFTVYLIGREA 401
Qy 373 SFADRMKWIACNKGYYTQISTLADTQENMEYLHLVLSRPMVINHDHDIWTEAYMDSKL 432
Db ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
402 AFADNLKWMACANKGPFPTQISTLADVQENWMEYLHLVLSRPMVINHDHDIWTEAYMDSKL 461
Qy 433 LSSQAQSLTLTTVAMPVFSKQNETRSHGILLGVGSDVALRELKMLAPRYKLGVHGYAF 492
Db ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
462 --ADDOGLVMTTVMPEVFSKQNETRSHGILLGVGSDVALRELKMLAPRYKLGVHGYAF 519
Qy 493 LNTNNGYILSHPDRLPLYREGKLPKPNYNSVDLSEVEWEDQAESLTAMINRETGTL 552
Db ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
520 AITNNGYILTHPELPLYESEKK--RRAPNTSSVDLSEVEWEDQAESLTAMINRETGTL 578
Qy 553 MDVKVPMKGRVFLTNDYFTDISDTPFSLGAVLSRGHGEYILLNGTSSVEEGLHDLHL 612
Db ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
579 MEVKKTVDKGRVLMVNTDYYTDIKGAPFSLGAVLSRGHGEYILLNGTSSVEEGLHDLHL 638
Qy 613 PDALAGDWIYCTDIDPHRKLSQLEAMIRFLTRKDPDLECDDELREVLFDVAVTAPM 672
Db ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
639 PDVSLADEWSYCNLTDLHPEHRHLSQLEAIKLYLKGKELPLQCDKELIQEVLFDVAVSAPI 698
Qy 673 EAYWTALALNMSBESEHVVDMAFLGTRAGLLRSSLFVSGSEKVSORKFLTPEDEASVFTLD 732
Db ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
699 EAYWTALALNMSBESEHVVDMAFLGTRAGLLRSSLFVSGSEKVSORKFLTPEDEASVFTLD 758
Qy 733 RFPLWYRAAEQIPGSPVYSIPFSTG--TVNKSNNVTASTSIQLLDERKSPVVAAGVQM 792
Db ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
759 RFPLWYRAAEQIPGSPVYSIPFSTG--TVNKSNNVTASTSIQLLDERKSPVVAAGVQM 816
Qy 793 KLEFLQKFWAATROCSVDGPTQSCDSLDLDFVINDNNGFILISKESRETGRFLGEVD 852
Db ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
817 KLEFLQKFWAATROCSVDGPTQSCDSLDLDFVINDNNGFILISKESRETGRFLGEVD 876
Qy 853 GAVLTQLLSMGVFSVOTWYDQAMCKPSSHHSAAOPLVSPISAFLTATRLMLLQELVFL 912
Db ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
877 GAVLTQLLSMGVFSVOTWYDQAMCKPSSHHSAAOPLVSPISAFLTATRLMLLQELVFL 936
Qy 913 LEWSVMSWYDGAERAKSFVHSHKHKKQDPLQPCDTEYVPVYQPAIREANGIVECGPC 972
Db ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
937 VEFNLC-SWVHSDMTAKA-----OKLKQTLPECDTEYPAFVSERTIKETGNIACBDC 988
Qy 973 QKVFVVOQIPNSNLLLVTDPTDCSIFPPVLQEADEVKNASVKCDMRMSOKLRRRPPDS 1032
Db ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
989 QKVFVVOQIPNSNLLLVTDPTDCSIFPPVLQEADEVKNASVKCDMRMSOKLRRRPPDS 1048
Qy 1033 CHAFHPEVVRVEADRGWAGFSS 1053
Db ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
1049 CHGFHPE---ENARECGASS 1066

RESULT 7
Q9NY16
ID Q9NY16 PRELIMINARY; PRT; 997 AA.
AC Q9NY16;

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DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Calcium channel alpha2-delta3 subunit.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Brain;
RC MEDLINE=21142395; PubMed=11245980; DOI=10.1016/S0378-1119(00)00600-4;
RA Hanke S., Bugert P., Chudek J., Kovacs G.;
RT "Cloning a calcium channel alpha2delta-3 subunit gene from a putative
RT tumor suppressor gene region at chromosome 3p21.1 in conventional
RT renal cell carcinoma.";
RL Gene 264:69-75(2001).
DR EMBL; AJ272268; CAB75962.1; -.
DR Genbank; HGNC:15460; CACNA2D3.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF02743; Cache; 2.
DR Pfam; PF00092; VWA; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS50234; VWFA; 1.
SQ SEQUENCE 997 AA; 112996 MW; B56D13133FD67B8D CRC64;

Query Match 56.8%; Score 3250.5; DB 2; Length 997;
Best Local Similarity 60.5%; Pred. No. 1.3e-188;
Matches 593; Conservative 177; Mismatches 191; Indels 19; Gaps 6;

QY 66 MENMLRRKRAVQNLVEAAEEADLNHEFNESLVFDYVNSVLINERDEKGNFVGLGAEFL 125
DB 1 MEEMFHKSSAVRLVPAEAAEHLKHEFDADLQYEFYNAVLIINERDKGNFLELGKEFIL 60

QY 126 ESNAHFSNLPVNTSISSVQLPTNVYKDPDILNGVYMSEALNAVVFENFORDPTLTWQYF 185
DB 61 APNDHFNNLPVNLSDVQVPTNMYNKDPALVNGVYWSLNVKVFVDNFDNDRDPSLIWQYF 120

QY 186 GSATGFPRIYPGIKWTDPDENGVTTFDCNRGWIQAATSPKDIIVLDVSGSMKGLRMTI 245
DB 121 GSAKGFPQYPGIKWEPDENGVIADFCDNRKRWYQAATSPKDVVILVDVSGSMKGLRLTI 180

QY 246 AKHTITITILTGENDPVNIAYNDVHYTEPCFKGLVQADNRNHRHFKLLVEELMVKG 305
DB 181 AKQTVSSILDTLGDGDDFNIIAYNEELHYEPCLUNGTLVQADRTNKEHREHLDKLFAKG 240

QY 306 VGVVDQALREAFQILKQFBAKQGSCLNQAIMLISDGADEYBPVEKYNWPPCKVRVFT 365
DB 241 IGLMDIALNEAFNLSDFNHTGQSGICSAQIMLITDGAVDYDTIFAKYNWPPCKVRIFT 300

QY 366 YLIGREVSFADRMKWIACNNKGYTQISTLADTQENVMYHLVLSRPMVINHDHDIWTE 425
DB 301 YLIGREAAFDNLKMWACANKGFFQTISTLADYQENVMYHLVLSRPMKVIDQEHVDVWTE 360

QY 426 AYWDKSLSSQAOSLT-----LLTTVAMPVFSKNSRSHGILLGVVGSDDVALRELMLK 479
DB 361 AYIDSTL--PQAQLTDQGPVLMTTVAMPVFSKQNETRSKGLLVGVVGTDPVPELTKT 418

QY 480 APRYKLGVHGYAFINTNNGYILSHPLDRLPYREGKKLKPKNYNSVDLSVEVEDQAESL 539
DB 419 IPKYKLGIHGAYFAITNNGYILTHPELRLLYEKGK--RRKPNSSVDLSVEVEDRDDVL 477

QY 540 RTAMINRETGLSMVKVPMDKGRVLFNTDYFFTDISTPFSLGAVLSRGHGEYLLG 599
DB 478 RNAMVNRKTKGFSNEVKTKVDKGRVLVMTNDYYTDIKGTFPSLGVALSRGHGKFFRG 537

QY 600 NTSVEGLHLLHPDLALAGDWYTCITDIDPHRKLSQLSEAMIRFTLRKPDLECEDELV 659
DB 538 NVTIEGLHLDHPDVSADENSYCNTDLHPEHRHLSQLSEAIKLYLKGKPEPLQCKDELI 597

QY 660 REVLFDVAVTPAMEAYWTALALNNSESEHVMDMAFLGTAGLLRSLSLFVGSEKVSORKF 719
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DB 598 QEVLEDAVVSAPIEAYWTSALANKSENSDKGVEVAFGLTRTGLSRINLFGAEQLTNQDF 657
QY 720 LTPEDASVFTLDRFPLWTRQASEHPAGSFVFNLRWAESEGESAGEPMVWTASTAVATVD 779
DB 658 LKAGDKENIFNADHPLWYRAAEQIPGSFVYSGIFSTGP--VNKSNVVTASTSIQLLDE 715
QY 780 KRTAIAAAGVOMKLEFLQRKFWAATRCQSTVDPYQTQSCEDSDLDLCFVDDNNGFILISK 839
DB 716 RKSPPVVAAGVQMKLEFFQKFWTASRQASLQKCSISCDDETVCYLIDNNGFILVSE 775
QY 840 RSRETGRFLGEVDGAVLTQLLSMGVFSQVMTYDQAMCKPSSHSHSAQAOLPVSIPASFLT 899
DB 776 DYTQTGDFGFEIEGAVNMKLLTWGSKFRITLYDQAMCRANKESSDCAHGLLDPNAPLS 835
QY 900 ATRWLLQELVLFLLEWSVWGSDYDRGAEAKSVFHHSHKHKQDPLQPCDTEYFVYVQPA 959
DB 836 AVKWMITELVLFLVEFNLC--SWHSDMTAKA-----QKLKOTLEPCDTEYPAFVSERT 887
QY 960 IREANGIVEGCGOKVFWQOIPNSNLLLVLTPTCDCSIFFPPVLQEADEVKYNASVKCD 1019
DB 888 IKETTGNIAECDCSKSFVQIIPSSNLFPMVVDSSCLCESVAPITMAPIRINYNESLKCE 947
QY 1020 RMRSQKLRRRPSDCHAFHPE 1039
DB 948 RLKAQKIRRRPESCHGFHPE 967

RESULT 8
Q9NY18
ID Q9NY18 PRELIMINARY; PRT; 519 AA.
AC Q9NY18;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Calcium channel alpha2-delta3 subunit.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=21142395; PubMed=11245980; DOI=10.1016/S0378-1119(00)00600-4;
RA Hanke S., Bugert P., Chudek J., Kovacs G.;
RT "Cloning a calcium channel alpha2delta-3 subunit gene from a putative
RT tumor suppressor gene region at chromosome 3p21.1 in conventional
RT renal cell carcinoma.";
RL Gene 264:69-75(2001).
DR EMBL; AJ272213; CAB75878.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF02743; Cache; 1.
DR Pfam; PF00092; VWA; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS50234; VWFA; 1.
SQ SEQUENCE 519 AA; 59526 MW; 198D13AF246286C6 CRC64;

Query Match 32.6%; Score 1866.5; DB 2; Length 519;
Best Local Similarity 68.9%; Pred. No. 6.1e-105;
Matches 344; Conservative 71; Mismatches 81; Indels 3; Gaps 2;

QY 66 MENMLRRKRAVQNLVEAAEEADLNHEFNESLVFDYVNSVLINERDEKGNFVGLGAEFL 125
DB 1 MEEMFHKSSAVRLVPAEAAEHLKHEFDADLQYEFYNAVLIINERDKGNFLELGKEFIL 60

QY 126 ESNAHFSNLPVNTSISSVQLPTNVYKDPDILNGVYMSEALNAVVFENFORDPTLTWQYF 185
DB 61 APNDHFNNLPVNLSDVQVPTNMYNKDPALVNGVYWSLNVKVFVDNFDNDRDPSLIWQYF 120

QY 186 GSATGFPRIYPGIKWTDPDENGVTTFDCNRGWIQAATSPKDIIVLDVSGSMKGLRMTI 245
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Db 121 GSAKFRQVPGIKWEPDENGVIAFDRCNRKWIQAATSPKVVILVDVSGSKMGLBLTI 180
 Qy 246 AKHTITITLDTLGNDFNIIAYNDYVHYIEPCFKGILVQADRONRSHFKLLVBEELMVKG 305
 Db 181 AKQTVSSILDTLGDGDDFNIIAYNEELHYVPECLNGTLVQADRNKSHFHEHLDKLFAKG 240
 Qy 306 VGVVDQALREAPQILKFOEAKQOSGLNQAIIMLISDGAVEDYEPFKYKYNWPCDKVRVPT 365
 Db 241 IGMULDIALNEAFNLISDFNHTGQSGISQAIIMLITDGAVDYDTIFAKYKYNWPCDKVRIFT 300
 Qy 366 YLIGREVSFADRMKWIACNNKGYTQISTLADTQENWVEYHLVLSRPMWLNHHDHDIWTE 425
 Db 301 YLIGREAFADNLKWKACANKGFTQISTLADVOENWVEYHLVLSRPMVDOEHVWVTE 360
 Qy 426 AYMDSKLLSSQAQSLTLLTIVAMPVFSKQNETRSHGILLGVGSDVALRELMLKAPRYKL 485
 Db 361 AYIDSTLTDQGP--VLMTTVAMPVFSKQNETRSGILLGVGTDVDPVKELLTKIPRYKL 418
 Qy 486 GVHGYAFINTNGVILSHPDRLPIYREGKLLKPKPNTNSVDLSEVEHEDQASLRTAMIN 545
 Db 419 GIHGAYAFATNNGVILTHPELRLLYEGRK-RRKPNYSYVDLSEVEHEDRDDVLRNAMVN 477
 Qy 546 RETGTLSDMDKVPMDKGR 564
 Db 478 RKTGKFSMEVKKTVDKGR 496

RESULT 9
 Q9V6T7 PRELIMINARY; PRT: 1218 AA.
 ID Q9V6T7 Q8T9C3;
 AC Q9V6T7, Q8T9C3;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE CG12295-P8 (SD07723p).
 GN ORFNames=CG12295;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=107311132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherter S.E., Li P.W., Hoekins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brannon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolehakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Buam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K.B., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Perriera S., Fleischmann W.,
 RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hootin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
 RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoekins R.A., Laverty T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richardson S., Sodergren E.J.,
 RA Svirkas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
 RT melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirkas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 RT a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo C., Pacleb J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; A5003617; AAF58335.2; -;
 DR EMBL; AY069830; AAL39975.1; -;
 DR FlyBase; FBgn0033870; CG12295.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR004010; Cache.
 DR InterPro; IPR002035; VWF_A.
 DR Pfam; PF02743; Cache; 2.
 DR Pfam; PF00092; VWA; 1.
 DR SMART; SM00327; VWA; 1.
 DR PROSITE; PS50234; VWFA; 1.
 SQ SEQUENCE 1218 AA; 140048 MW; 4F04224063D527B5 CRC64;

Query Match

27.1%; Score 1551; DB 2; Length 1218;

Best Local Similarity 33.0%; Pred. No. 3,2e-85;		Matches 397; Conservative 207; Mismatches 365; Indels 234; Gaps 43;	
Qy	13	VKLWADTFGDLNTVNTYKYSGLLLQKYYKDVSSLLKIEV---DGLYLRKRSDEMNM	69
Db	40	VHSWADKLGMELF-----HLGDFLTR--KEVQESFKDAKVVRNGASIVDSMAKEIEM	92
Qy	70	LRRKVEAQVQLVFAAEADLNHEFN-BSLVDFYNSVLINERDEKGNFV-----	117
Db	93	MDLKVSAVRIMDTAENTASHQNDMADKMFYSYA---KEMLEPGDPVPIPTPADMD	149
Qy	118	-ELGAEL-----LESNAHFSNLPVNTSISVOLPTVYNNKDDPLNGVYMSEALNA	168
Db	150	KDICEPLIYQPKVVVLEPRPEFHNTPVNFSVSVSHVNVFDRAPDVIKAIQWSENLDQ	209
Qy	169	VFVENFORDTLTWQYFGSATGFPRIYPGIKWTPDENGVITFDNRNGWYIQATSPKDI	228
Db	210	IFRDNKNDPTLSQWFGSGTGMFRQPPASKWRKDV--PVDLYDCRLSWMYMEATSPKI	268
Qy	229	VILVDVSGSMKGLRMTIAKHTITITLTLGENDPVNIIAYNDVYHYIEPCFKGILVQADR	288
Db	269	VILMDGSSMLGQELDIAKHVNTILDTLTGNDVFNIFTDKEVSPVPVPCFETLQANL	328
Qy	289	DNREHFLLVIELVMVGKGVVQALREAFQILKQFQAKQSGSLCNOAIMLISDCAVEDYE	348
Db	329	GNIRELKEGIELPRKSIANYTAALTAKAFELLEETKLSSRGAOCNOAIMIIGDAPENNR	388
Qy	349	PVEKYNW---PCKVRVFTLYLGREVSFADRMKWIACNNKGYTQISTLATQENWMEY	405
Db	389	EVFELHNWRDPYKPVRFVFTLYLGKEVANWDDIRWMACENQGYVHLSDTAEVREVMVNY	448
Qy	406	LHVLRSRPMVI-NHDHDIIMTEAYMD-----	434
Db	449	IPWAPLVLGRHDHPVINSQVADIEDTKLSYLDINDINOCEYQKADVLEYWQVHDMLE	508
Qy	435	S-----QAQSLTLTTTAMPVFSKKNETRSHGILLGVGSDVALRE	475
Db	509	PSEMHRKRYRMKETWNPQVDSNVYQPMTVSPNPIVDRRENATRIANILVAGTDVPINE	568
Qy	476	LMKLAPYKLVGKYGAFPLNTNGVILSHDPLRYREGKLLKPKPNVNSVDLSEVWEDQ	535
Db	569	IKLLSPFTLVNGYAFIVTNGVLFHPDFRPIF-QGYILKFA--YNSVDMLEVLDD	625
Qy	536	AE-----SLRTAMINRETGTLSDMVKVPMDKGRVFLTNDYFFDDISDTPFSLG	585
Db	626	DRAPDNVPLMTIRDSIIINQSGKMWLVKNHFDKMRVARVKRYQYWTAIKKTFTLV	685
Qy	586	AVLSRGHG-----EYILLGNT---SVEEGLHDLHLPLDALAGMWIYCIITDIP	630
Db	686	ISYPEQYGVSHMDIRADOETHRISIKGTNLSRVFSGRWKIHP-----DMLFC-----	733
Qy	631	DHR-----KLSQLEAMIRPLTRKD-----PD-----LECDLELVREVLFDVAV	668
Db	734	KHSNRTFKTPEIE-LIYFELRMESEPGWRWPGSSAMPPEHAAMFCDRQLMQALVFDARV	792
Qy	669	TAPWEAYWTA--LALANSESEHV-----VDMAFGLTRAGLRSLSF---VGSEKVSOR	717
Db	793	TG-----WFSNNTSFNSKDKNGEFKQRFQVTVAFATLATHSGLTRWHEFHSNAAEESGVGE	847
Qy	718	KFTPDEASVFTLDRPLWYRQA-SH--PAGSFVFNLRWAGSPSAGE---PMVVTAS	771
Db	848	TF-----SQNNTRAIDE--IWYKRAVDQHFRVEESFVYSV-----PFDAGSSEILVTAS	896
Qy	772	TAVAVTVKBTATAAAGVQMKLEFLQRFKFWAATRCQSTVDGPTYQSCEDSDLDGCFIDN	831
Db	897	HAFVHNEGKGTAPAAVVGFOFQHSALYKLFPHNTGNACAVD-----DKDCYILDN	946
Qy	832	NGFILSKRSRETGRFLGVDGAVLTQLLSGMVFSQVMTYDYQAMCKPSSHHSAAQPLV	891
Db	947	NGVVIISVTRVHETGRPFGEVNGAIMKLELLENVYRVQTVYDQAVCFESKNDNNASSMLL	1006
Qy	892	SPISAFLTATRWLLOELVLF---LLEWS--VWGSWVDRGAEKSV-----FHSHK	937

Db	1007	SPLFHLRLRVGKWLHTALWYIVQLQWAPGVSSHYADMYGDSNDTEPPPPPHDPDHARN	1066
Qy	938	---HKQDP-----LQPCDTEYVPVYQPAFREANGIV---ECGPCQKVFVY	978
Db	1067	GNHGKGDHDDHWIRYITLHRTLKPCDMKRDLYT---LFNEKDNVYVNTMTAHACERPFVY	1123
Qy	979	QQIPNSNLLLLVTDPTC--DCSIFPPVLQEATE--VKYNASVKCDRMRSQKLRRRPDSC	1034
Db	1124	LPFPNSNLLLLVTDQCPDGSVVLTWNPQIDYHLSVNDSLACYKQAREFNMRPHSCI	1183
Qy	1035	AFH 1037	
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DT	01-MAR-2003 (TEMBLrel. 23, Created)		
DT	01-MAR-2003 (TEMBLrel. 23, Last sequence update)		
DT	01-MAR-2004 (TEMBLrel. 26, Last annotation update)		
DE	CG12455-PB.		
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OS	Drosophila melanogaster (fruit fly)?		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydroidea; Drosophilidae; Drosophila.		
OX	NCBI_TaxID=7227;		
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RA	Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,		
RA	Amanatides P.G., Scherz S.E., Li P.W., Hoskins R.A., Galle R.F.,		
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,		
RA	Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,		
RA	Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,		
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,		
RA	Abriel J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,		
RA	Balaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,		
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,		
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,		
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,		
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RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,		
RA	Fosler C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,		
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,		
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,		
RA	Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,		
RA	Talali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,		
RA	Kimball B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,		
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,		
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,		
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,		
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,		
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,		
RA	Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,		
RA	Reinert K., Remington I., Saunders R.D., Scheeler F., Shen H.,		
RA	Shue B.C., Siden-Kianos I., Simpson M., Skupski M.P., Smith T.,		
RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,		
RA	Swirekas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,		
RA	Wang Z.Y., Wasarman D.A., Weinstein G.M., Weissenbach J.,		
RA	Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,		
RA	Yeh R.F., Zaveri J.S., Zhan M., Zhang Q., Zhao Q., Zheng L.,		
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,		
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;		
RL	"The genome sequence of Drosophila melanogaster.";		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=22426065; PubMed=12537568;		

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OX Eohydroidea; Drosophilidae; Drosophila.
RN NCBI_TaxID=7227;
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RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
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RA Foeller C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
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RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
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RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Rainert K., Remington K., Saunders R.D., Scheier F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zhang R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*
RT *melanogaster* euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426072; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.A., Campbell K.S.,
RA Hradscky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RN [7]
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RC STRAIN=Berkley;
RX MEDLINE=99403001; PubMed=10471707;
RA Ashburner M., Misra S., Roote J., Lewis S.E., Blazey R., Davis T.,
RA Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,
RA Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
RA Palazzolo M., Reese M.G., Spradling A., Teang G., Wan K., Whitelaw K.,
RA Celniker S., Rubin G.M.;
RT "An exploration of the sequence of a 2.9-Mb region of the genome of
RT *Drosophila melanogaster*: the Adh region.";
RL Genetics 153:179-219(1999).
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazey R.G.,
RA Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
RA Farnon D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
RA Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
RA Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
RA Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
RA Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,
RA Zieran L.L., Rubin G.M.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [9]
DR ENBL; AB003650; AAF53505.2; -
DR ENBL; AB003415; AAF4988.1; -
DR FlyBase; Fggn0028859; CGI2455.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF02743; Cache; 1.
DR Pfam; PF00092; VWA; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS0234; VWFA; 1.
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Query Match 25.2%; Score 1441; DB 2; Length 2190;
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Matches 378; Conservative 187; Mismatches 373; Indels 234; Gaps 44;
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QY 125 LESNAHFNLPVNTSISVOLPTNVNKPDPDILGVYMSALNAVVFENFQDPDTLTWOY 184
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QY 185 FGSATGFFRIYPIGKWT---PDENGVIITFCRNRGWYIQAAATSPKDIIVLVDSYSGMKGL 241
DB 198 FGSDTGILRHYPAAQWTDTRPNRDDADTVDCRKSRYETATCTSKDVIILLDHSGSGTGF 257
QY 242 RMTIAGHTTTTLDTUGENDFNVIAYNDYVHYIECFKGLIVQADRDNREHFALLVEEL 301
DB 258 RHHVAKFTIRSLDFTLNNDFFTLIRYSSEVNDIIFCPNGALVQATPENIEVFNQIQIEQL 317


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Qy 357 -----PDCKVRVFTYLGREVSPADRMKWTACHNKGYYTQISTLAQTQENVMYLVLS 410
Dy 378 NGENGTOMTRVFTYLLGKEVTKREIQOMACLNRGYISHVQTLDEHVEVLKYVDVIA 437
Qy 411 RPMVI-NHDDIHWTEAYMSKL--LSSQAQSLTLTTVAMPVFSK-----KNETRSHGIL 463
Dy 438 TPLVLQNEHQPTWTHAFTDXTYDPTKSNEKRPRLMISGVGPAFDRFYRHANSTNPRARL 497
Qy 464 LGVVGSDVALBELMKLAPRYKLGHVGAFLTNNGYILSHPDRLPLRYREGKKLKPKNYN 523
Dy 498 LGVAGTDPVEDIDIKLTPYKLGNGYSFVSNNGYVLLHPDLRPIGTNGKM---NPNYN 554
Qy 524 SVDLSEVE--WEDQA-----ES---LRTAMINRETGTL-SMDVKVPMDKGRVLFNLNDY 572
Dy 555 SIDTVEVHLFEDQSPREPGEIHLIRNAMVRHEANFEKSIKVFHYDKMKRRVSEEKQDY 614
Qy 573 FTDISDTPFSLGAVLSRGHGE-YILLG-----NTSVEEGLHDL-----LHPDLALAG 619
Dy 615 FFAPLNTPTFLGIVMPSEYSGKTWKVGEVVDKXHKMKINISDFFIGENMKVHP----- 668
Qy 620 DWIYCIITDIDPDHKKLSOLEAMIR-FLTRKDDPLE-----LHPDLALAG 619
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Qy 654 -----CDEELRVFLDVAVTAPMEAYWTALANMSESEHV-----VDMFLGTRAGLL 703
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Dy 1054 YTVHEDLS-DIDTGNHAKQHKDSFPNPSNG 1084
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AC Q70758
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE AGCP5954 (Fragment).
GN Name=agCG56326; ORFName=ENSGG00000018729;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR GO: AAAB01008960; EAA10906.1; -.
DR GO: GO:0016020; C-membrane; IEA.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF02743; Cache; 1.
DR Pfam; PF00092; VWA; 1.
DR PROSITE; PS0234; VWA; 1.
FT NON_TER 1
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SQ SEQUENCE 1028 AA; 118517 MW; 5A6E0DA689ABCF9 CRC64;
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Query Match 25.0%; Score 1430.5; DB 2; Length 1028;
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Matches 349; Conservative 181; Mismatches 333; Indels 191; Gaps 29;

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Qy 70 LRBEKVAQNLVEAASEADLNHEFNSLV---FDYNSVLINERDEKGNFVEL----- 119
Dy 57 MDAKVSARKIMDTAENTAIS--FDEEPVNSQFOYNA---KOMIEPEEITTPIMIDE 111
Qy 120 -----GABFLLESNAHFNLPVNTSISSVQLPTNVNKPDPDILNGVYMSEALNAV 169
Dy 112 DPADITTPPPKGIIVLTKKRHFNEAVNTTVSSVHVPTNVYDRATEVTEIKAKSEALDSI 171
Qy 170 FVENFORDPTLTWQYFGSATGFPRIYPIGKIWTDPENGVIITFDNCRNGWYIQAATSPKDIV 229
Dy 172 FYNNYIGDPTLTWQYFGSSGFLRPFPATKW--EQDPVDLYDCRLRSWYIEAANSKMDL 229
Qy 230 ILVDVSGSMKGLRMTAKHTITTLTGLGDNFVNIAYNDVHYIEPCFKILVQADRD 289
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Qy 290 NREHFKLLVBEELMVGVVDQALREAFQILKQFOEAKQSLCNQAIMLISDGAVEDYEP 349
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Dy 350 VFEQFNWKLPTFPVRVFTYLGREVADVKEIKEMACRNGQYVHLSVMAEVRREVLYNI 409
Qy 407 HVLSRPMVNL-HDHDIIWTEAYND-----SKLL----- 433
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Qy 477 MKLAPRYKLGHVGAFLTNNGYILSHPDRLPLRYREGKKLKPKNYNVDLSEVWED-- 534
Dy 530 KKYLPKHLGNGVYAFIVTNNGYILTHPDPRPVQD-----ILKPAVNTVDWIEVELTDDD 585
Qy 535 -----CAESLRTAMINRETGTLSDVCKPMDKGRVLFNLNDYFFTDISTPESLGA 586
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Qy 625 ---ITDIDPHRKLQSLEAM-----IRELTRKDPD-----LECOBELVREVLFAVVTPAM 672
Db 698 HPNETFATPELELKHFLERMKLGWKWPSNRTPPPEHAMFCDEGLMQALVYDAKTEWF 757
Qy 673 EAYWTALANMSSESHV-----VDMAPLQTRAGLRRSLF---VGSEKVSRRKFLTPED 724
Db 758 SKNVSGSGGNKDEKGNBFKORFGITVGSFLATHSGLTRWQBYATGADESKQAEPDFSETHN 817
Qy 725 EASVFTLDRPPLMYROASE-----HAGSFFVFNLRWAGPESAG-- 763
Db 818 RA-----VYTRAVELYYSNRNKGADGKNGKDDSRNSFVSV-----PFDAGNR 866
Qy 764 EPMVVTASTAVAVTVDKRTAIAAAGVQMKLEFLQRFKFAATRCQSTVDGPTQSCBDS 823
Db 867 NDTLVATASHAIFHADGAREAPVAVGFPFHSAALYTLFKNITSQCGHGDPRCEKTCFTGD 926
Qy 824 LDCFVDNNGFILLKRSRETGRPLGVDGAVLTQLLSMGVFSQVTVTYDYQAMCKSPSSH 883
Db 927 YQCVVIDNNGFVISEQLQETGAFFGVEKPAFMQRLDDSIERNVTYDYQAVCFMAKGS 986
Qy 884 HSAQAQLVSPISAFLTATRLMLQELVLFLEWSV 917
Db 987 INLGTVLQTP-----LRLWMLLTNTFTSYLV-WVV 1015

RESULT 13
Q7PM00
ID Q7PM00 PRELIMINARY; PRT; 1011 AA.
AC Q7PM00;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP0000020925 (Fragment).
GN Name=ENSANGSG0000018436;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR ENBL; AAB01008980; EAA14572.2; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF02743; Cache; 1..
DR Pfam; PF00092; VWA; 1..
DR PROSITE; PS0234; VWFA; 1.
FT NON_TER 1011 1011
SQ SEQUENCE 1011 AA; 117662 MW; 70C7D6B71CC93E59 CRC64;

Query Match 24.4%; Score 1398; DB 2; Length 1011;
Best Local Similarity 33.2%; Pred. No. 4.8e-76;
Matches 340; Conservative 184; Mismatches 351; Indels 150; Gaps 32;

Qy 16 WADTFGGDLVNTVTKYSGSLLLQKKYKDVBSLKIIEVDGLVLRKFSEDMENLRKRYE 75
Db 4 WADNFGELWDLAQTTKAMEITAKYKAYNA--RVEHKDGTALIQSIVENVRGMFIRKMD 61
Qy 76 AVQNLVEAAEADLNHEFNSLV--FDYNSVLIN-----ERDEKGNFVE---LGAEFLL 125
Db 62 AIKCIINLAEELSEQEFNETLADNFSYSSKYSNIDGRPEPIPETLQENMMMYRNMSL 121
Qy 126 ESNAHFSNLPVNTSISVOLPTVYVKNKDPDILNGVYMSALNAVVFENFORDPTLTWQYF 185
Db 122 NPTHEFNISVNTSYSGVHPQVNYDRYPWVLEALQWSLDDVFLQYNSDPAISWQYF 181
Qy 186 GSATGFFRIYPGIKWTPDENGVITFCRNRGWYQAATSPKQIVILVDVSGSMKGLRMTI 245
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Db 182 GSYTGMLRHPALEWNRH--VDTFDCRKSWEIETATCSKOIVILLDNSGSMGYRNYI 239
Qy 246 AKHTITITLDTLGENDFVNIANDVHYIEPCFK-----GI 282
Db 240 AQLTVKSIILDTFSNDFINIYKYSNDVEPLVPCFKVGLKILDEKCNRVRFNNTSLSLQDM 299
Qy 283 LVQADRDNRHPKLLVVEELMVKGVVVDQALREAFQILKQFQEAQK---GSLCNOAIML 338
Db 300 LVQATPENWRFFNEYVRELLPEGYANVKAFVAAFELLQYRIIRRCNVSVCNQAIML 359
Qy 339 ISGAVEDYEPVPEKYNW----PDCKRVFTYILIGREVSFADRMKIACNKGYYTQIST 394
Db 360 ITDGVPSNITEVEFAYNWFENGTKIPRVFTYLLGREVTKVREIQMACLNRGYSHIQS 419
Qy 395 LADTQENWYELHLSRPMVINH-DHDIITWEAYMDS--KLL--SSQAQSLTLTTVTAMP 449
Db 420 LDEVOEVLKYYVTIATPLVLQGVHEPPTWTHAFTDAENLLTEADDEPRLMIAYGAP 479
Qy 450 VFSKK---NETRSHGILLGVGSDVALRELMLAPRYKLGVHGVAFLNTNNGYILSHPD 505
Db 480 AFDKKNHYNETRT--ARLLQVAGTDIPVEDLDLTLPYKLGVNGYSFIVSNGYVLMHPD 538
Qy 506 LRPLYREGKLLKPKPNYNSVDLSEVW-----EDQAE-----SLRTAMINRE 547
Db 539 LRPV-----SNGRLKENYSIDLTEIEQIYDENITROIEDMTGREMSPFILELRQLHVDQS 594
Qy 548 TGTLS-MDKVPMDKGRVLFNTDYPFTDIDSPTPSLGAVALSRHGE--YILG-----N 600
Db 595 FGNMTKLPVRFHYDKMRRVSLQYQYVYAPLENTPFSLGLVLPDHYGSTMWIKVGEIKRN 654
Qy 601 TSVEEGLHDL-----LHPDLALAGDWLYCITDIDPDHRKLSQLEAMIRFLTR----- 647
Db 655 QHMLNISDFPMGDNWKVHP-----DWYCKHYLEGHEFTKPEDELRFHLNRLYEPTW 708
Qy 648 -----KDPLECEDEELVREVLFDVAVVTAPMEAYWTALALN 682
Db 709 KWSQQVEPEPNKESDGPNCGRKTLDDDAYCNKELVQLLIPDAKVTNNSYRNWF---- 764
Qy 683 MSESEHVVDM-----AFLGTRAGLLRSSLFVSGEKV-SDRKFLTPEDASVTLDRFPL 736
Db 765 ENENERKIIEMYNATLRFVATMSGLTRWQFI FGEVEVDTDSDFGYHKA-----IDE--T 818
Qy 737 WYRQA--SEHPAG--SPVFNLRWAGPESAGEPMVVTASTAVAVTVDKRTAIAAAGVQMK 793
Db 819 WYRSAILQHKIDPKSFVSPHESDPEDGE-LKVTAATWAIIPRDCGLEAPGCVTGFQFT 877
Qy 794 LEFLQKRFWAATRCQSTVDGPTQSCESDLDLQCFVINDNNGFILLKRSRETGRFLGEVDG 853
Db 878 HSLMYDRFMEITSK-TTCDG-CIETCASESRDCYVIDHNGYVVLSETSNHTGRFFGEIEG 935
Qy 854 AVLTQLLSMGVFSQVTVTYDYQAMCKPSSHHSAAQPLVSPISAFLTATRLMLQELVFL 913
Db 936 AIMQSMVDKEIFTMTITVFDLQGLCEYERVVENDATALLHPMKVFMGLKWLTAIEAIMLS 995
Qy 914 EWSVW 918
Db 996 RFDWF 1000

RESULT 14
Q9NK83
ID Q9NK83 PRELIMINARY; PRT; 1255 AA.
AC Q9NK83;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein BG:DS07108.2.
GN Name=BG:DS07108.2; ORFNames=CG4587;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
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OX NCBI_TaxID=7227;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=99403001; PubMed=10471707;
RA Ashburner M., Miera S., Rote J., Lewis S.E., Blazej R., Davis T.,
RA Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,
RA Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
RA Palazzolo M., Reese M.G., Spradling A., Teang G., Wan K., Whitelaw K.,
RA Celnikier S., Rubin G.M.;
RT "An exploration of the sequence of a 2.9-Mb region of the genome of
RL Drosophila melanogaster: the Adh region.";
RN Genetics 153:179-219(1999).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Celnikier S.E., Agbayani A., Arcalana T.T., Baxter E., Blazej R.G.,
RA Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
RA Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
RA Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
RA Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
RA Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
RA Sethi H., Snir E., Svirskaas R.R., Wan K.H., Weinburg T., Zhang R.,
RA Zieran L.L., Rubin G.M.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003413; AAP44957.1; -
DR FlyBase; FBgn0028663; CG4587.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF02743; Cache; 1.
DR Pfam; PF00092; VWA; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS0234; VWFA; 1.
KW Hypothetical protein.
SQ SEQUENCE 1255 AA; 140745 MW; FEB584D76C7785C6 CRC64;

Query Match 22.8%; Score 1305.5; DB 2; Length 1255;
Best Local Similarity 29.1%; Pred. No. 2.8e-70;
Matches 328; Conservative 203; Mismatches 403; Indels 195; Gaps 30;

QY 80 LVEAREAEADLNHPENSLV-----FDYNSVLINERDEKGNFVELGAELLESNAHFSN 133
DB 116 LMSAEQAALSELEGGQAEPMGGQOQHYDARRINEYNADGKLADGARHDIRFMRFR 175

QY 134 LPVNTSSVOLPTNPNKOPDIILGVYMEALNAVVENFORDPTLTQYFGSATGFFR 193
DB 176 LPVNLSSILVPHGVLDDEPDVKSALQWSGHLDPFQNNLEQDPALSWQYFGSGTFLR 235

QY 194 IYPIGIKTPD--ENGVTTPCNRNGWYQIATSPKDIIVLDVSGSMKGLRMTIAKHTIT 251
DB 236 RFPCTAWPPEGSKGLIHDFTHTNFWVQAASSPKDIMILLDASSMTSEKSFGLGMATAF 295

QY 252 TILDTLGENDFVNIANDVYHYIEPCFGLVQADRDREHFKLLVLEELMWKGVGVDDQ 311
DB 296 NILDTLGEDDFVNLITFSEVVVKTVPVCFKORMVRATPDNTQETIKSAKAIKQDNTANFTA 355

QY 312 ALREAFOILQFOBAKQSGSLCNOAIMLISGAVDYEPVFEKYNWPCVKRVFTYLIGRE 371
DB 356 GLEYAFSELLKXNKGAGSCNQAIMLITSTSESHKDVIKQYNWHPMVRIFTYLIGSD 415

QY 372 VSFADRMKVIACNNKGYTQISTLADTQENVMYELHVLSPMVI-NHDDHIITWEAYMDS 430
DB 416 SGSRSLNLDHMACSKNGFFVQINDYDEARRKVIDYALVMARPMIYQADHPVHNSPVFVAG 475

QY 431 K---LLSSQAQLTLLTIVAMPVSKNERTSHGILLGVGSDVALBELMKLAPRYKLV 487
DB 476 KSGGLGRDSEYQRRLVTTVSTVPFDRNRHNSVRVANLLGVGVDVPIEIRKVPQHKLGP 535

QY 488 HGVAFLTNNGYILSHLDPLRYREGKLL-KPKPNYNSVDLSEVEM----- 532
DB 536 NGYSFIVDNGRVLVHPLDPLGDANQYIDQLKPKYASVDITELPELPETFGNNPEIEI 595

QY 533 -BDQASLSRTAMINRETGTLSMDVKVPMQKGRVLFITNDYFPTDTSDFSLGAVLSRG 591
DB 596 NKLLNEMRGDMIKPKGEGETEFTVMNHYDDSKRVSTRTHRYFYGPIDETFTLAILVPEK 655

QY 592 HGVYILLGNTSVSEGLHDL-----LHPDLALAGDWIYC-----ITDIDPDHKLQSO 637
DB 656 YGSHFVSQOEIRHSNNVTVEYFKGDNWRVHP-----DWYCEYNSVSLERKRESSGE 709
QY 638 L-----EAMIRFL-----TRKOPDLE 653
DB 710 YSSRDQEPSFGSPPEQVRPKSPQHNNMHSNGNAPGSSSHFGSOHOSQGSRAEPYF 769
QY 654 CDEELVREVLFDVAVTAPMEAYWTALANMSESE-----HYVDMAFGLTGRLLRSLFV 709
DB 770 CDRALLQLSVRDAMVTDGLDNTTSSGSGKEDQOQYQKVFVATSFVATSSGLLR---WI 826

QY 710 GSKVSDRKFLTPE---DEASVFLDRFPLWYQOA-SEHPA---GSFVFLNRWAEGPSAG 763
DB 827 DHVK---REDTPEPHFSEDNVRAMD--TSWYKRAIDQHSVEPDSFVYSPFGSGYAIKS 881
QY 764 EPMVTVASTAVTVVDKRTAIAAAAGVQMKLEFLQRKFWAATQCSTVDGPGYTQSCDSD 823
DB 882 NATLVATASHAIFVEHRGHKAAAGVWGLQFQHDLSLAKHFINITSACTGWTG-CKRTCASDN 940

QY 824 LDCFVIDNNGFILI SKRSRETGFLGEVDCAVLTQLLSMGVFSQVTVMYDYQAMCKPSSH 883
DB 941 LDCYVLDSGFIISSEMEHTKFGFGIDGTDLSLVQDRIYKRVTVNDYQGVCSADNP 1000

QY 884 HSAAQPLVSPISAFLTATATRLQLLQELVLFLEW-----S 916
DB 1001 YTAAGGILKP---NRLGSWFFNHLLSALSAWLSLMPASLRAMPQEBYTYDNEVDVFDN 1056
QY 917 VNGSWYDRG-----ABAKSVFHHSHKHK-----KODP--LQPCD 948
DB 1057 NYSDEVEFGNENYNNQVQDQEMDEFETTADVEYTTTPPRQHKPHVGRFSPDPHNARRCD 1116

QY 949 TEPVVFYQPAIREANG-----IVEC---GPCQKVFVQQIIPNSNLLLVLTDTCDCC- 997
DB 1117 LRTDLYMLOPERLUNQOGQNNPLKGLTNCVSCERPFSVQKIPHSNLLLVLTDTLPCPG 1176

QY 998 ----STFPVPLQBATKYNASVKCDRMR---SQKLRRRRPSCHAFHPE 1039
DB 1177 SKQLDIEP--LEBAGVIG-----ACSTRQGOQESRRRPPKKNYHPE 1218

RESULT 15
Q9VJN7
ID Q9VJN7 PRELIMINARY; PRT; 1120 AA.
AC Q9VJN7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG4587-PA.
GN ORPNames=CG4587;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Gabor G.L.,
RA Abrial J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Borchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodeon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foeller C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yen R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA "The genome sequence of *Drosophila melanogaster*.";
RA Science 287:2185-2195(2000).
RN [2]
RX SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.B.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RA "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*
RA *melanogaster* euchromatic genome sequence.";
RA Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RX SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RA "The transposable elements of the *Drosophila melanogaster* euchromatin:
RA a genomics perspective.";
RA Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RX SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RA "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RA systematic review.";
RA Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RX SEQUENCE FROM N.A.
RX FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RX SEQUENCE FROM N.A.
RX FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; AE003648; AAF53476.2; -;
DR FlyBase; FBgn028863; CG4587.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR04010; Cache.

DR InterPro; IPR002035; VWF_A.
DR Pfam; PF02743; Cache; 1.
DR Pfam; PF00092; WVA; 1.
DR SMART; SM00327; WVA; 1.
DR PROSITE; PS0234; VWFA; 1.
SQ SEQUENCE 1120 AA; 126057 MW; F409EA40BB601F3F CRC64;
Query Match 22.4%; Score 1283; DB 2; Length 1120;
Best Local Similarity 28.9%; Pred. No. 5.5e-69;
Matches 318; Conservative 196; Mismatches 383; Indels 202; Gaps 29;
QY 101 YNSVLINERDERGNFVFLGAEFLLESNAHFNLSNPVNTSISSVQLPTNVYKDPDILNGV 160
DB 27 HYDARRINEADGKLGADGARHMDIRFMRFRFLPNVLSLSILVPHGVLDLDEPDVKSAL 86
QY 161 YNSEALNAVVENFQDPDTLTWQYFGSATGFFRIYIGIKWTPD--ENGVTFFDCRNGWY 218
DB 87 QNSGHLDPLEQNNLEQDPALSWQYFGSSTGFLRFRFGTAWPPGSGSKLIHDFRTHWF 146
QY 219 IQAATSPKDIVILVDVSGSMKGLRMTIAKHTITITLDTLGENDFVNIAYNDVYHYIEPC 278
DB 147 VQASSPKDILMLLDASSMTEKSFDLGNATAFNILDTLGEDDFNLTSEVVKTVPVC 206
QY 279 FKGILYQADRDNRHFKLLVEELMVGVGVVDOALREAFQILKQFOEAKOGSLCNOAIML 338
DB 207 FKDRVVRATPDNIQEIKSAVKAIKLDQTANFTAGLEVAFSLHLKYNQSGAGSCNQAIML 266
QY 339 ISDGAVEDYEPVEKYNWPDCKVRVTYLLIGREVSFADRMKWIACNNKGYTYQISTLADT 398
DB 267 ITESSEHKDVIKQYNWPHMPVRIPTYLLIGSDSGSRSLNLDHMACSKNGKPFVQINDYDEA 326
QY 399 QENVMYLVLSRPMVI-NHDDHIIWTEAVMDSKLLSSQAQSLTLLTTVAAMPVFSKKNET 457
DB 327 RRKVIDYALVWAPRMVYQADHPVHWSPVFV-----AVSTPVPDRNHS 370
QY 458 RSHGILLGVGSDVALREMLKAPRYKLGVHGVAFLNTNNGYILSHPDRLPLYREGKKL- 516
DB 371 VRVANLLGVGTDVPTEIRKVPQHKLGPNGSFYVDNNGRVLYHPDLRPLGDANQYID 430
QY 517 KPKPNYSVDLSREVW-----EDQAESLRTAMINRETGTLSDMVKVPMDK 561
DB 431 QLKPKPYASVDITELPETEFGNNEPFIENKLLNLMERGDMIKPKEGETEFTVMNHYDD 490
QY 562 GKRVLFTNDYPTDTSDFPSLGAVLSRGHGVIYLLGNTSVBEGLHDL-----L 611
DB 491 SKRVSTRTHRYFYGPIDPTFTLAIIVLPEKYSHEFVSQOEIRHSRNVVTEYFGDNWRV 550
QY 612 HPDLALAGDWIYC---ITDIDPDHRLKLSQL-----EAMIRFL----- 645
DB 551 HP-----DWVYCEYNSVDLEKERESSGSEYSSRDQEPSFGSPQVPRKSPQHNMHS 604
QY 646 -----TRKDPDLECEDELREVLFDVAVTAPMEAYVTALALNM 683
DB 605 GSNNGNAPGSHFGSQHQSQRKAEPYFCDRALLQSLVRDAMVTDGLDRNTTGSSESGK 664
QY 684 SESE-----HVVDMAFLGTRAGLLRSSLVFGSKVSDRKLTPPE---DEASVFTLDRFPL 736
DB 665 EKQOQYQKVVATSFVATRSGLLR---WIDHVK---RPEDTEPHFSEDNVTRAMD--TS 716
QY 737 WYRQA-SEHPA--GSVFNLRWAGPESAGEPMVVTASTAVAVTVDKRTAIAAAGVQMK 793
DB 717 WYKRAIDQHSVEPDSFVSVFPGSGYAIKSNATLVTAASHAI FVEHGHKAAGAAGVVGLOFQ 776
QY 794 LEPLOKFWAATROCSTVDGPTYQSCEDSDLCFVIDNNGFILI SKRSRTGTFGLBEVDG 853
DB 777 HDSLAKHFNITSACTGMTG-CRKT CASDNLDCYILDNSGFVIISEMEHTKFFPGQIDG 835
QY 854 AVLTQLLSMGVFSQVTMYDQAMCKPSHHSAAOPLVSPISAFATATRLQLQELVLFLL 913
DB 836 TMDLSLVQDRIYKRVTVNDYQGVCSADPNPYTAAGGILKP-----NRLGSHFFNHLALS 891
QY 914 EW-----SVNGSWYDRG-----AE 927

```
Db      892  A W L S L M P A S L R A W P Q E E Y T Y D N E D V F V D N N Y S D E Y E F G N E N E Y N M Q V D Q E M D E F F T T A D 951
Qy      928  A K S V F H H S H K H K - - - - - K Q D P - - L Q P C D T E Y P V F V Y Q P A I R E A N G - - - - - I V E C - 969
Db      952  V E Y T P P P R Q H K P H V G P R F S P D P H N A R C D L R T D L Y M L Q P E R L N Q G G N N P L K G K L T N C H 1011
Qy      970  - G P C Q K V F V Q Q I P N S N L L L V T D P T C D C - - - - - S I F P P V L Q E A T E Y K Y N A S V K C D R M R - 1022
Db      1012 V S G C E R P F S V Q K I P H S N L L I L L V D T L C P C G S K Q L D I E P - - L E E A G V I G - - - - - A C S T R R Q 1064
Qy      1023 - - S Q K L R R R P D S C H A F H P E 1039
Db      1065 G Q E Q E S R R R P K K C I N Y H P E 1083
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Search completed: November 16, 2005, 03:22:51
Job time : 196 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 16, 2005, 19:23:23 ; Search time 1314 Seconds

(without alignments)
4910.592 Million cell updates/sec

Title: US-09-833-222A-10

Perfect score: 5726

Sequence: 1 MAVALGTRRRDRYKVLADTF.....MPMTPVPVVLGGNIRYAL 1090

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh

-Q=/cgn2_1/USPTO_spool_h/US09833222/runat_15112005.145357.15779/app_query_faeta_1.1287

-DB=N_Geneseq -QMT=fascap -SURFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOPEXT=0

-UNITS=bits -START=1 -END=-1 -MATRIX=blom62 -TRANS=human40.cdi -LIST=45

-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL

-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000

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-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG

-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: Geneseq16Dec04.*

2: Geneseq1980s.*

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4: Geneseq2000s.*

5: Geneseq2001as.*

6: Geneseq2001bs.*

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8: Geneseq2002bs.*

9: Geneseq2003as.*

10: Geneseq2003bs.*

11: Geneseq2003cs.*

12: Geneseq2003ds.*

13: Geneseq2004as.*

13: Geneseq2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5726	100.0	3486	10	ADF71819 Human cal
2	5726	100.0	3486	10	Abz20598 Human vol
3	5386.5	94.1	5073	3	Aaa09254 Human alp
4	5385.5	94.1	4841	10	Ade07110 Novel cod
5	5342.5	93.3	3339	4	AAS01433 Human sec

6	5342.5	93.3	3339	5	AAf57570	Aaf57570 Human cal
7	5276	92.1	3209	4	AA01432	Aa01432 Human sec
8	5276	92.1	3209	5	AAf57569	Aaf57569 Human cal
9	5234.5	91.4	3228	6	AA017581	Aa017581 DNA encod
10	5230.5	91.3	3345	6	AA017582	Aa017582 DNA encod
11	5197.5	90.8	5713	3	AA09278	Aa09278 Human alp
12	5148	89.9	3201	4	AA01431	Aa01431 Human sec
13	5148	89.9	3201	5	AAf57568	Aaf57568 Human cal
14	5127.5	89.5	3742	13	ADN33188	Adn33188 Human tra
15	3808	66.5	4125	6	AA022004	Aa022004 Human cal
16	3416.5	59.7	3690	6	AA026399	Aa026399 Human cal
17	3410.5	59.6	3770	3	AA09253	Aa09253 Human alp
18	3410.5	59.6	3770	4	AA01414	Aa01414 Human sec
19	3410.5	59.6	3770	5	AAf57551	Aaf57551 Human cal
20	3400.5	59.4	3213	4	AA01409	Aa01409 Human sec
21	3400.5	59.4	3213	5	AAf57546	Aaf57546 Human cal
22	3326.5	58.1	3114	4	AA01408	Aa01408 Human sec
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24	3278.5	57.3	3057	4	AA01407	Aa01407 Human sec
25	3278.5	57.3	3057	5	AAf57544	Aaf57544 Human cal
26	3222	56.3	3598	3	AAA09261	Aa09261 Human alp
27	3195.5	55.8	3382	8	ABZ23112	Abz23112 Nucleotid
28	2306	40.3	1523	10	ADK41000	Adk41000 Novel hum
29	2306	40.3	1523	13	ADR15714	Adr15714 Kinase 41
30	2218	38.7	1452	3	AAA09279	Aa09279 Human alp
31	2026.5	35.4	2008	3	AA09260	Aa09260 Human alp
32	1959.5	34.2	1774	3	AAZ51626	Aaz51626 Human mem
33	1792.5	31.3	1050	4	AA01412	Aa01412 Human sec
34	1792.5	31.3	1050	5	AAf57549	Aaf57549 Human cal
35	1695	29.6	969	4	AA01411	Aa01411 Human sec
36	1695	29.6	969	5	AAf57548	Aaf57548 Human cal
37	1598	27.9	912	4	AA01410	Aa01410 Human sec
38	1598	27.9	912	5	AAf57547	Aaf57547 Human cal
39	1565	27.3	4892	12	AD016904	Ado16904 Tobacco b
40	1554.5	27.1	5028	12	AD016902	Ado16902 Tobacco b
41	1497.5	26.2	5862	5	AA05208	Aa05208 D. melano
42	1410	24.6	6519	4	ABL22283	AbL22283 Drosophil
43	1392.5	24.3	4383	12	AD016900	Ado16900 Tobacco b
44	1362.5	23.8	856	4	AAS31088	Aas31088 Human dia
45	1336.5	23.3	3414	4	ABL10835	AbL10835 Drosophil

ALIGNMENTS

RESULT 1

ADF71819

ID ADF71819 standard; cDNA; 3486 BP.

XX

AC ADF71819;

XX

DT 12-FEB-2004 (first entry)

XX

DE Human calcium channel alpha2delta4 subunit cDNA.

XX

XX neuroprotective; cytosolic; gene therapy; calcium channel;

KW alpha2delta-4; amyotrophic lateral sclerosis; multiple sclerosis; cancer;

KW human; gene; ss.

XX Homo sapiens.

OS

XX Key Location/Qualifiers

FT CDS 190..3462

FT /*tag= a

FT /product= "Human calcium channel alpha2delta4 subunit"

XX

PN US2003170785-A1.

XX

PD 11-SEP-2003.

XX

PF 10-APR-2002; 2002US-00119624.

XX

PR 11-APR-2001; 2001US-00833222.

XX

PA (QINN//) QIN N.
PA (CODD//) CODD E.
PI Qin N, Codd E;
XX
DR WPI; 2003-898262/82.
DR P-PSDB; ADF71820.
XX
XX New human alpha2 delta4 calcium channel subunit protein and nucleic acid
PT molecule, useful for diagnosing and treating diseases associated with
PT defective calcium channel subunit, e.g. cancer and multiple sclerosis.
XX
XX Claim 10; SEQ ID NO 9; 37pp; English.
XX
XX The invention describes a new isolated and purified nucleic acid molecule
CC comprising: a sequence having at least a 70% identity to nucleotides 1-
CC 224 or 3308-3486 of a sequence of 3486 bp (Sl) fully defined in the
CC specification; at least 15 sequential bases of the polynucleotide of (a);
CC or a sequence that is complementary to the polynucleotide of (a) or (b).
CC Specifically claimed is an alpha2delta-4 nucleic acid molecule comprising
CC a sequence of 3486 bp fully defined in the specification and encoding an
CC alpha2delta-4 calcium channel subunit protein having a sequence of 1090
CC amino acids fully defined in the specification. The nucleic acid molecule
CC and polypeptide are useful in diagnosing and treating a disease or
CC disorder associated with a defective alpha2delta-4 subunit, such as
CC ankyrotrophic lateral sclerosis, multiple sclerosis or cancer. The methods
CC may be used for identifying compounds capable of treating the above-
CC mentioned diseases or disorders. This sequence encodes human calcium
CC channel alpha2delta-4 subunit.
XX
SQ Sequence 3486 BP; 827 A; 957 C; 1009 G; 693 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 3486
Score: 5726.00 Matches: 1090
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-833-222A-10 (1-1090) x ADF71819 (1-3486)

QY 1 MetAlaValAlaLeuGlyThrArgArgAspArgValLysLeuTrpAlaAspThrPhe 20
Db 190 ATGGCTGTACTTTAGGCAACAGGAGGAGGAGAGAGTGAAGTATGGGCTGACACCTTC 249

QY 21 GlyGlyAspLeuTyrAsnThrValThrLysTyrSerGlySerLeuLeuGlnLysLys 40
Db 250 GGCGGGGACCTGTATAACACTGTGACCAATACTCAGGCTCTCTTTGCTGCAGAGAAG 309

QY 41 TyrLysAspValGluSerSerLeuLysLysLysLysLysLysLysLysLysLysLys 60
Db 310 TACAAGATGTGGAGTCCAGTCTGAAGATCGAGAGGTGGATGGCTTGGAGCTGGTGAGG 369

QY 61 LysPheSerGluAspMetGluAsnMetLeuArgArgLysValGluAlaValGlnAsnLeu 80
Db 370 AAGTTCTCAGAGGACATGGAGAACATGCTGCGAGGAGNAAGTCAGGCGGTCCAGATCTG 429

QY 81 ValGluAlaAlaGluAlaAspLeuAsnHisGluPheAsnGluSerLeuValPheAsp 100
Db 430 GTGGAAGCTGCCGAGGAGGCGGACCTGAAACACGAATTCATGAATCCCTGGTGTTCGAC 489

QY 101 TyrTyrAsnSerValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 120
Db 490 TATTACAACTCGGTCTCTGATCAACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 549

QY 121 AlaGluPheLeuLeuGluSerAsnAlaHisPheSerAsnLeuProValAsnThrSerIle 140
Db 550 GCCGAGTTCCTCTCGGAGTCCAATGCTCACTTCAGCAACCTGCCGCTGAACACCTCCATC 609

QY 141 SerSerValGlnLeuProThrAsnValTyrAsnLysAspProAspIleLeuAsnGlyVal 160
Db 610 AGCAGCGTGCAGCTGCCCAACGTTGTACAAACAAAGAGCCAGATATTTTAAATGGAGTC 669

QY 161 TyrMetSerGluAlaLeuAsnAlaValPheValGluAsnPheGlnArgAspProThrLeu 180
Db 670 TACATGTCTGAAGCCTTGAATGCTGTCTTGGTGGAGAACTTCAGAGAGACCCCAACGTTG 729

QY 181 ThrTrpGlnTyrPheGlySerAlaThrGlyPhePheArgIleTyrProGlyIleLysTrp 200
Db 730 ACCTGGCAATATTTGGCAGTGCACCTGGATCTTTCAGGATCTATCCAGGTATAAATGG 789

QY 201 ThrProAspGluAsnGlyValIleThrPheAspCysArgAsnArgGlyTrpTrpIleGln 220
Db 790 ACACCTGATGAGAATGGAGTCACTTACTTTGACTGCCGAACCGCGCTGCTGATCAATCAA 849

QY 221 AlaAlaThrSerProLysAspIleValIleLeuValAspValSerGlySerMetLysGly 240
Db 850 GCTGCTACTTCTCCCAAGGACATAGTATTTTGGTGACGTGAGCGGAGATATGAAGGG 909

QY 241 LeuArgMetThrIleAlaLysHisThrIleThrThrIleLeuAspThrLeuGlyGluAsn 260
Db 910 CTGAGGATGACTATTGCCAAGCACACCATCACCACCATCTTGGACACCTTGGGGGAGAT 969

QY 261 AspPheValAsnIleIleAlaTyrAsnAspTyrValHisTyrIleGluProCysPheLys 280
Db 970 GACTTCGTTAATATCATAGCTACATGACTACGTCCATTACATCGAGCCTTGTGTTAAA 1029

QY 281 GlyIleLeuValGlnAlaAspArgAsnArgGluHisPheLysLeuLeuValGluGlu 300
Db 1030 GGATCCTCGTCAGCGGAGCAGACATCGAGACATTTCAACTGCTGTGGAGGAG 1089

QY 301 LeuMetValLysGlyValGlyValValAspGlnAlaLeuArgGluAlaPheGlnIleLeu 320
Db 1090 TTGATGGTCAAGAGTGTGGGGTGTGGACCAAGCCCTCAGAGAAAGCTTCCAGATCCTG 1149

QY 321 LysGlnPheGlnGluAlaLysGlnGlySerLeuCysAsnGlnAlaIleMetLeuIleSer 340
Db 1150 AAGCAGTTTCCAAGAGGCCAAGCAAGAAAGCCTCTGCAACAGAGCCATCATGCTCATCAGC 1209

QY 341 AspGlyAlaValGluAspTyrGluProValPheGluLysTyrAsnTrpProAspCysLys 360
Db 1210 GACGGCGCGTGGAGGACTACGAGCGCGTGTGAGAAATATTAACCTGGCCAGACTGTAA 1269

QY 361 ValArgValPheThrTyrLeuIleGlyArgGluValSerPheAlaAspArgMetLysTrp 380
Db 1270 GTCCGAGTTTTCACCTTACCTCATTTGGGAGAGAGTGTCTTTTGTCCACCGCATGAAGTG 1329

QY 381 IleAlaCysAsnAsnLysGlyTyrTyrThrGlnIleSerThrIleAlaAspThrGlnGlu 400
Db 1330 ATTGCATGCAACCAACAAAGGCTACTACAGCGAGATCTCAACGCTGGCGGACACCCAGGAG 1389

QY 401 AsnValMetGluTyrLeuHisValLeuSerArgProMetValIleAsnHisAspHisAsp 420
Db 1390 AACGTGATGGAAATCCTGCACTGCTCAGCGCCCATGGTCAATCAACACAGACACGAC 1449

QY 421 IleIleTrpThrGluAlaTyrMetAspSerLysLeuLeuSerSerGlnAlaGlnSerLeu 440
Db 1450 ATCATCTGACAGAGGCTTACATGGACAGCAAGCTCCTCAGCTCGCAGGCTCAGAGCCTG 1509

QY 441 ThrLeuLeuThrThrValAlaMetProValPheSerLysLysAsnGlnThrArgSerHis 460
Db 1510 ACACCTGCTCACCACCTGTGGCCATGCGAGTCTTTCAGCAAGAAACGAAACGCGATCCCAT 1569

QY 461 GlyIleLeuLeuGlyValValGlySerAspValAlaLeuArgGluLeuMetLysLeuAla 480
Db 1570 GGCATTTCTCTGGGTGTGGGCTCAGATGTGGCCCTCAGAGAGGCTGATGAAGCTGGCG 1629

QY 481 ProArgTyrLysLeuGlyValHisGlyTyrAlaPheLeuAsnThrAsnAsnGlyTyrIle 500
Db 1630 CCCCAGTCAAGCTGGAGTGCAGCATACGCTTTCTGAAACACCAACCAATGGCTACATC 1689

QY 501 LeuSerHisProAspLeuArgProLeuTyrArgGluGlyLysLysLysLysLysLysLys 520
Db 1690 CTCTCCCATCCGACCTCCGGCCCCCTGTATCAGAGAGGGGAGAAACTAAACCCCAACCT 1749

Qy 521 AsnTyrAsnSerValAspLeuSerGluValGluTrpGluAspGlnAlaGluSerLeuArg 540
Db 1750 AACTACAAACAGTGTGGATCTCTCCGAAGTGGAGTGGGAAGACCAAGGCTGAATCTCTCAGA 1809
Qy 541 ThrAlaMetIleAsnArgGluThrGlyThrLeuSerMetAspValLysValProMetAsp 560
Db 1810 ACAGCCATGATCAATAGGAAACAGGTACTCTCTCGATGGATGTGAAGGTTCCGATGGAT 1869
Qy 561 LysGlyLysArgValLeuPheLeuThrAsnAspTyrPhePheThrAspIleSerAspThr 580
Db 1870 AAAGGAAGCGAGTCTTTCTCCGACCAATGACTACTTCTTCCAGGCATCAGCGACACC 1929
Qy 581 ProPheSerLeuGlyAlaValLeuSerArgGlyHisGlyGluTyrIleLeuLeuGlyAsn 600
Db 1930 CCTTTCAGTTGGGGGGGGTGTCTCTCCGGGGCCACCGAGAATACATCTCTTCTGGGGAAC 1989
Qy 601 ThrSerValGluGluGlyLeuHisAspLeuLeuHisProAspLeuAlaLeuAlaGlyAsp 620
Db 1990 ACGTCTGTGGNAGAGGCTGCGATGCTTGTCTTCCAGCAGACTGGCCCTGGCCGGTGAC 2049
Qy 621 TrpIleTyrCysIleThrAspIleAspProAspHisArgLysLeuSerGlnLeuGluAla 640
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Qy 641 MetIleArgPheLeuThrArgLysAspProAspLeuGluCysAspGluLeuValArg 660
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Qy 661 GluValLeuPheAspAlaValThrAlaProMetGluAlaTyrTrpThrAlaLeuAla 680
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Qy 681 LeuAsnMetSerGluGluSerGluHisValValAspMetAlaPheLeuGlyThrArgAla 700
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Qy 761 SerAlaGlyGluProMetValValThrAlaSerThrAlaValAlaValThrValAspLys 780
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Qy 861 SerMetGlyValPheSerGlnValThrMetTyrAspTyrGlnAlaMetCysLysProSer 880
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Qy 881 SerHisHisSerAlaAlaGlnProLeuValSerProIleSerAlaPheLeuThrAla 900

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Db 2890 ACCAGGTGGTGTCTGCAGGAGCTGGTGTCTTCTGCTGGAGTGGAGTGTCTGGGGCTCC 2949
Qy 921 TrpTyrAspArgGlyAlaGluAlaLysSerValPheHisHisSerHisLysHisLysLys 940
Db 2950 TGGTACGACAGAGGGCCGAGGCCAAAAGTGTCTTCCATCACTCCCAACCAACAAGAAG 3009
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Qy 961 ArgGluAlaAsnGlyIleValGluCysGlyProCysGlnLysValPheValValGlnGln 980
Db 3070 CGGGAGGCCAACGGATCGTGGAGTGGGGCCCTGCCAGAAAGGTATTTGTGGTCAGCAG 3129
Qy 981 IleProAsnSerAsnLeuLeuLeuValThrAspProThrCysAspCysSerIlePhe 1000
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Qy 1001 ProProValLeuGlnGluAlaThrGluValLysTyrAsnAlaSerValLysCysAspArg 1020
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Qy 1041 ArgValGluAlaAspArgGlyTrpAlaGlyPheSerSerProAsnProLeuCysLeuGly 1060
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Qy 1061 LeuCysProCysArgGlnGluHisIleGlyMetProMetAsnThrProValProValLeu 1080
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Qy 1081 LeuGlyGlyAsnIleArgValTyrAlaLeu 1090
Db 3430 CTGGGGGAAACATTCCGGTTTATGCCCTG 3459
RESULT 2
ABZ20598
ID ABZ20598 standard; cDNA; 3486 BP.
XX AC ABZ20598;
XX 03-MAR-2003 (first entry)
XX Human voltage gated calcium channel alpha2delta-4 subunit cDNA.
DE Human; voltage gated calcium channel; alpha2delta-4 subunit;
KW antiparkinsonian; tranquilizer; neuroprotective; anticonvulsant;
KW antimigraine; analgesic; cytostatic; antidepressant; antiinflammatory;
KW gene therapy; epilepsy; migraine; ataxia; vestibular defect;
KW chronic pain; neuropathic pain; Parkinson's disease; depression; cancer;
KW inflammation; seizure-related syndrome; anxiety; multiple sclerosis; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 190..3462
XX /*tag= a
XX /product= "calcium channel alpha2delta-4 subunit"
XX WO200283947-A2.
XX 24-OCT-2002.
XX 10-APR-2002; 2002WO-US011297.
XX

PR 11-APR-2001; 2001US-00833222.
 XX (ORTH) ORTHO-MCNEIL PHARM INC.
 PA
 PI Qin N, Codd E;
 XX WPI; 2003-093006/08.
 DR P-PSDB; ABP59509.
 XX
 PT New nucleic acid molecule encoding human alpha2 delta4 calcium channel
 subunit protein, useful for diagnosing and treating a disease associated
 PT with defects in the subunit protein, e.g. epilepsy, migraine, ataxia or
 PT chronic pain.
 XX
 PS Claim 1; Page 56-59; 91pp; English.
 XX
 CC The present invention provides the protein and coding sequences of human
 CC voltage gated calcium channel alpha2delta-4 subunit. The sequences are
 CC useful for diagnosing and treating a disease or disorder associated with
 CC a defective alpha2delta-4 subunit, such as seizure-related syndromes,
 CC epilepsy, migraine, ataxia, vestibular defects, chronic pain, neuropathic
 CC pain, mood, sleep interference, anxiety, AIDS, multiple sclerosis, mania,
 CC Parkinson's disease, substance abuse/addiction syndromes, depression,
 CC cancer, or inflammation. The present sequence is the coding sequence of
 CC the invention
 XX
 SQ Sequence 3486 BP; 827 A; 957 C; 1009 G; 693 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0 Length: 3486
 Score: 5726.00 Matches: 1090
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0
 US-09-833-222a-10 (1-1090) x ABZ20598 (1-3486)
 Qy 1 MetAlaValAlaLeuGlyThrArgAtgAspArgValLysLeuTrpAlaAspThrPhe 20
 Db |||||
 Qy 190 ATGGCTGTAGCTTTAGGGA CAAGAGGAGGAGAGTGAAGCTATGGGCTGACACCTTC 249
 Db |||||
 Qy 21 GlyGlyAspLeuTrpAenThrValThrLysTrpSerGlySerLeuLeuLeuGlnLysLys 40
 Db |||||
 Qy 250 GGCGGGACCTGTATAACACTGTGACCAATATCTCAGGCTCTCTCTTGCTGCGAGAGAG 309
 Db |||||
 Qy 41 TyrLysAspValGluSerSerLeuLysIleGluGluValAspGlyLeuGluLeuValArg 60
 Db |||||
 Qy 310 TACAAGGATGTGGAGTCCAGTCTGAAGATCGAGGAGGTGGATGGCTTGGAGCTGGTGAGG 369
 Db |||||
 Qy 61 LysPheSerGluAspMetGluAenMetLeuArgArgLysValGluAlaValGlnAenLeu 80
 Db |||||
 Qy 370 AAGTTCTCAGAGACATGGAGAACATGCTCGGAGGAGAAAGTCAGGCGGTCCAGAAATCTG 429
 Db |||||
 Qy 81 ValGluAlaAlaGluGluAlaAspLeuAenHisGluPheAenGluSerLeuValPheAsp 100
 Db |||||
 Qy 430 GTGGAAGCTGCCGAGGCGGACCTGACCAACGAATTCATGAATCCCTGGTGTTCGAC 489
 Db |||||
 Qy 101 TyrTyraenSerValLeuIleAenGluArgAspGluLysGlyAenPheValGluLeuGly 120
 Db |||||
 Qy 490 TATTACAACCTCGGTCTGTATCAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 549
 Db |||||
 Qy 121 AlaGluPheLeuLeuGluSerAenAlaHisPheSerAenLeuProValAenThrSerIle 140
 Db |||||
 Qy 550 GCCAGTTCTCTGGAGTCCAATGCTCTCTTCAACCACTCGCGGTGAACACCTCCATC 609
 Db |||||
 Qy 141 SerSerValGlnLeuProThrAenValTyrAenLysAspProAspIleLeuAenGlyVal 160
 Db |||||
 Qy 610 AGCAGCGTGCAGCTGCCCAACGCTGTACAAACAAAGAGCCAGATATTTAATATGAGTC 669
 Db |||||
 Qy 161 TyrMetSerGluAlaLeuAenAlaValPheValGluAenPheGlnArgAspProThrLeu 180
 Db |||||
 Qy 670 TATATGTCTGAAGCCTTGAATGCTGCTTCTGTTGAGAACTTCCAGAGAGACCCCAACGTTG 729
 Db |||||

Qy 181 ThrTrpGlnTyrPheGlySerAlaThrGlyPhePheArgIleTyrProGlyIleLysTrp 200
 Db |||||
 Qy 730 ACCTGGCAATATTTGGCAGTGCACCTGGATTCTTCAGGATCTATCAGGATATAAAATGG 789
 Db |||||
 Qy 201 ThrProAspGluAenGlyValIleThrPheAspCysArgAenArgGlyTyrTrpIleGln 220
 Db |||||
 Qy 790 ACACCTGATGAGAAATGAGTCACTTTTGAATGCGGAAACCGCGGTGTATCAATCAA 849
 Db |||||
 Qy 221 AlaAlaThrSerProLysAspIleValIleLeuValAspValSerGlySerMetLysGly 240
 Db |||||
 Qy 850 GCTGCTACTTCTCCCAAGGACATAGTCAATTTTGGTGACGTCGAGCGCAGTATGAAGGG 909
 Db |||||
 Qy 241 LeuArgMetThrIleAlaLysHisThrIleThrIleLeuAspThrLeuGluAen 260
 Db |||||
 Qy 910 CTGAGGATGACTTATGCCCAAGCACCATCACCACCATCTTGGACACCTCGGGGAGAAAT 969
 Db |||||
 Qy 261 AspPheValAenIleAlaTyrAenAspTyrValHisTyrIleGluProCysPheLys 280
 Db |||||
 Qy 970 GACTTCGTTAATATCATAGGTAATGACTACGTCCATTTACATCGAGCCTTGTTTTAA 1029
 Db |||||
 Qy 281 GlyIleLeuValGlnAlaAspArgAspAenArgGluHisPheLysLeuValGluGlu 300
 Db |||||
 Qy 1030 GGGATCTCTGCTCCAGCGGACCGAGACAATCGAGAGCATTTTCAAACTGCTGGTGGAGG 1089
 Db |||||
 Qy 301 LeuMetValLysGlyValGlyValValAspGlnAlaLeuArgGluAlaPheGlnIleLeu 320
 Db |||||
 Qy 1090 TTGATGTCAAAGGTGTGGGTCTGGACCAAGCCCTTGAGAAAGCCTTCAGATCCTG 1149
 Db |||||
 Qy 321 LysGlnPheGlnGluAlaLysGlnGlySerLeuCysAenGlnAlaIleMetLeuIleSer 340
 Db |||||
 Qy 1150 AAGCAGTTCCAAAGAGGCCAAGCAAGAGCCTCTGCAACCCAGGCCATCATGCTCATCAGC 1209
 Db |||||
 Qy 341 AspGlyAlaValGluAspTyrGluProValPheGluLysTyrAenTrpProAspCysLys 360
 Db |||||
 Qy 1210 GACGGCGCTGGAGGACTACGAGCGGTGTTTGAAGATATAACTGGCCAGACTGTGAAG 1269
 Db |||||
 Qy 361 ValArgValPheThrTrpLeuIleGlyArgGluValSerPheAlaAspArgMetLysTrp 380
 Db |||||
 Qy 1270 GTCCGAGTTTTCACCTTACCTCATTTGGGAGAGAGTGTCTTTTGTCTGACCGCATGAAGTGG 1329
 Db |||||
 Qy 381 IleAlaCysAenAsnLysGlyTyrTrpThrGlnIleSerThrLeuAlaAspThrGlnGlu 400
 Db |||||
 Qy 1330 ATTGCATGCAACAAACAAAGGCTACTACACGAGATCTCAACGCTGGCGGACACCCAGGAG 1389
 Db |||||
 Qy 401 AenValMetGluTyrLeuHisValLeuSerArgProMetValIleAenHisAspHisAsp 420
 Db |||||
 Qy 1390 AACGTGATGGAATACCTGCACGCTGCTCAGCCGCCCATGGTCTCATCAACCAACGACCGAC 1449
 Db |||||
 Qy 421 IleIleTrpThrGluAlaTyrMetAspSerLysLeuLeuSerSerGlnAlaGlnSerLeu 440
 Db |||||
 Qy 1450 ATCATCTGACAGAGAGCCCTACATGGACACAGCTCTCTCAGCTCGAGGCTCAGAGCCTG 1509
 Db |||||
 Qy 441 ThrLeuLeuThrThrValAlaMetProValPheSerLysAenGluThrArgSerHis 460
 Db |||||
 Qy 1510 ACACTGCTCACCATGTGTGCCCATGTCAGTCTTCAGCAAGAAGAACGAAACCGCATCCCAT 1569
 Db |||||
 Qy 461 GlyIleLeuLeuGlyValValGlySerAspValAlaLeuArgGluLeuMetLysLeuAla 480
 Db |||||
 Qy 1570 GGCATTCTCTGGGTGTGGTGGCTCAGATGTGGCCCTGAGAGAGTGTGAAGAGCTGGCG 1629
 Db |||||
 Qy 481 ProArgTyrLysLeuGlyValHisGlyTyrAlaPheLeuAenThrAenAenGlyTyrIle 500
 Db |||||
 Qy 1630 CCCCCGTACAGCTTGGAGTGCAGGATAGCTCTTCTGAACACCAACCAATGGCTACATC 1689
 Db |||||
 Qy 501 LeuSerHisProAspLeuArgProLeuTyrArgGluGlyLysLysLysProLysPro 520
 Db |||||
 Qy 1690 CTCTCCATCCGACCTCCGGCCCTGTACAGAGAGGAGGAGAACTAAACCCCAACCT 1749
 Db |||||
 Qy 521 AenTyrAenSerValAspLeuSerGluValGluTrpGluAenGlnAlaGluSerLeuArg 540
 Db |||||
 Qy 1750 AACTACACAGTGTGATCTCTCCGAAGTGGAGTGGGAAGACGAGCTGAATCTCTGAGA 1809
 Db |||||

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Qy 541 ThrAlaMetIleAenArgGluThrGlyThrIleuSerMetAspValIysValProMetAsp 560
Db 1810 ACAGCCATGATCAATAGCGAAACAGGTACTCTCTCGATGGATGTGAAGGTTCCGATGCAT 1869
Qy 561 LysGlyValArgValLeuPheLeuThrAsnAspTyrPhePheThrAspIleSerAspThr 580
Db 1870 AAAGGAAGCGAGTTCCTTCTGACCAATGACTACTTCTTCAGGACATCAGGCACACC 1929
Qy 581 ProPheSerLeuGlyAlaValLeuSerArgGlyHisGlyGluTyrIleLeuLeuGlyAsn 600
Db 1930 CCTTTCAGTTGGGGCGGTGCTGTCGGGGCCACCGGAGATACATCCTTCTGGGGAAC 1989
Qy 601 ThrSerValGluGluGlyLeuHisAspLeuLeuHisProAspLeuAlaLeuAlaGlyAsp 620
Db 1990 ACGTCTGTGAAGAAGCCCTGCTGACTTGTCTTCCACCCAGACCTGGCCCTGGCCGTGAC 2049
Qy 621 TrpIleTyrCysIleThrAspIleAspProAspHisArgIysLeuSerGlnLeuGluAla 640
Db 2050 TGGATCTACTGCATCAGAGATATTGACCCAGACCACCCGGAAGCTCAGCCAGCTAGAGGCC 2109
Qy 641 MetIleArgPheLeuThrArgLysAspProAspLeuGluCysAspGluGluLeuValArg 660
Db 2110 ATGATCCGCTTCTCACCAGGAAGAGCCAGACCTGGAGTGTGACGAGGAGCTGGTCCGG 2169
Qy 661 GluValLeuPheAspAlaValValThrAlaProMetGluAlaTyrTrpThrAlaLeuAla 680
Db 2170 GAGGTGCTGTTGACGGCGGTGTGACAGCCGCCATGGAAGCCTACTCGACAGCGCTGGCC 2229
Qy 681 LeuAsnMetSerGluGluSerGluHisValValAspMetAlaPheLeuGlyThrArgAla 700
Db 2230 CTCACATGTCCGAGGAGTCTGAACACGTGTGTGACATGGCCCTTCTCGGGCACCCGGGCT 2289
Qy 701 GlyLeuLeuArgSerSerLeuPheValGlySerGluLysValSerAspArgLysPheLeu 720
Db 2290 GGCTCTCTGAGAACAGCTGTTGCTGGGGTCCGAGAGGTCCTCCGACAGAGATTCCTG 2349
Qy 721 ThrProGluAspGluAlaSerValPheThrIleuAspArgPheProLeuTyrTrpThrArgGln 740
Db 2350 ACACCTGAGGACGAGGCGAGCGTGTTCACCCCTGGACCGCTTCCCGCTGTGTGATACCGCAG 2409
Qy 741 AlaSerGluHisProAlaGlySerPheValPheAsnLeuArgTrpAlaGluGlyProGlu 760
Db 2410 GCCTCAGAGCATCTGCTGGCAGCTTCTGTTCAACCTCCGCTGGGCGAGAGGACCCAGAA 2469
Qy 761 SerAlaGlyGluProMetValValThrAlaSerThrAlaValAlaValThrValAspLys 780
Db 2470 AGTGGGGTGNACCCATGGTGGTGACCGCAAGCACACGCTGTGGCGGTGACCGTGGACAAG 2529
Qy 781 ArgThrAlaIleAlaAlaAlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLys 800
Db 2530 AGGACAGCCATTGCTGCAGCGCGGGCGTCCAAATGAAGCTGGAATTCCTCCAGCGCAAA 2589
Qy 801 PheTrpAlaThrArgGlnCysSerThrValAspGlyProTyrThrGlnSerCysGlu 820
Db 2590 TTCTGGGGCGGAACCGCGCAGTGCAGCAGCTGTGGATGGGCGGTACACACAGAGCTGGAG 2649
Qy 821 AspSerAspLeuAspCysPheValIleAspAsnAsnGlyPheIleLeuIleSerLysArg 840
Db 2650 GACAGTGATCTGGACTGCTTCGTCATCGACACACAAACGGGTTCATTCTGATCTCCAAGAGG 2709
Qy 841 SerArgGluThrGlyArgPheLeuGlyGluValAspGlyAlaValLeuThrGlnLeuLeu 860
Db 2710 TCCCGAGAGACGGGAAGATTCTGGGGAGGTGGATGGTGTCTCTGACCCAGCGCTGCTC 2769
Qy 861 SerMetGlyValPheSerGlnValThrMetTyrAspTyrGlnAlaMetCysLysProSer 880
Db 2770 AGCATGGGGTGTTCACCGCAAGTACTATGATGACTATCAGGCCATGTGCAAAACCCCTCG 2829
Qy 881 SerHisHisSerAlaAlaGlnProLeuValSerProIleSerAlaPheLeuThrAla 900
Db 2830 AGTCACCACACAGTCAGCGCCACGCCCTGTGTGAGCCCAATTTCTGCTCTTGTGACGGCG 2889
Qy 901 ThrArgTrpLeuLeuGlnGluLeuValLeuPheLeuLeuGluTrpSerValTrpGlySer 920
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Db 2890 ACCAGGTGGCTGCTGCAGGAGCTGGTGTCTCTGCTGCAGTGGAGTGTCTGGGGCTCC 2949
Qy 921 TrpTyrAspArgGlyAlaGluAlaLysSerValPheHisHisSerHisLysHisLysLys 940
Db 2950 TGGTACGACAGAGGGCGGAGGCCAAAGTGTCTTCATCTACTCCCAACAACAACAAG 3009
Qy 941 GlnAspProLeuGlnProCysAspThrGluTyrProValPheValTyrGlnProAlaIle 960
Db 3010 CAGGACCCGCTGCAGGCCCTCGCACACGGAGTACCCCGTGTTCGTGTACCAAGCCGCCATC 3069
Qy 961 ArgGluAlaAsnGlyIleValGluCysGlyProCysGlnLysValPheValGlnGln 980
Db 3070 CGGAGGCCAACGGGATCGTGGAGTGGGGCCCTGCCAGAAAGTATTTGGTGCAGCAG 3129
Qy 981 IleProAsnSerAsnLeuLeuLeuValThrAspProThrCysAspCysSerIlePhe 1000
Db 3130 ATTCCCAACAGTAACCTCTCTCTGCTGCAGAGCCCCACCTGTGACTGCAGCATCTTC 3189
Qy 1001 ProProValLeuGlnGluAlaThrGluValLysTyrAsnAlaSerValLysCysAspArg 1020
Db 3190 CCACCAAGTGTGCAGGAGGCGACAGAAATCAATATAATGCCTCTGTCAAAATGTGACCGG 3249
Qy 1021 MetArgSerGlnLysLeuArgArgProAspSerCysHisAlaPheHisProGluVal 1040
Db 3250 ATGCGCTCCAGAAAGCTCCGCGGCGACCAAGCTCTCTGCCACGCCCTTCCATCCAGAGGTG 3309
Qy 1041 ArgValGluAlaAspArgGlyTrpAlaGlyPheSerSerProAsnProLeuCysLeuGly 1060
Db 3310 CGGGTTGAGGCGGATCGAGGGTGGGTGGATTTTCATCCCAAAACCCCTCTGTGCTGGGT 3369
Qy 1061 LeuCysProCysArgGlnGluHisIleGlyMetProMetAsnThrProValProValLeu 1080
Db 3370 CTGTGCCCCCTGCAGACAGGAGCATATAGGATGCCAATGAACACACACCTGTGCTGTGCTT 3429
Qy 1081 LeuGlyGlyAsnIleArgValTyrAlaLeu 1090
Db 3430 CTCGGGGGAAACATTCCGCTTTATGCCCTG 3459

RESULT 3
AAA09254
ID AAA09254 standard; cDNA; 5073 BP.
XX AAA09254;
XX XX
DT 10-AUG-2000 (first entry)
XX XX
DE Human alpha-2-delta-D gene.
XX XX
KW alpha-2-delta-D; calcium channel; 12p13.3; gabapentin; cytostatic;
KW anticonvulsant; antimigrane; antiparkinsonian; antidepressant; ss.
XX XX
OS Homo sapiens.
XX Key Location/Qualifiers
FT CDS 3..3365
FT FT /*tag= a
PN WO200020450-A2.
XX XX
PD 13-APR-2000.
XX XX
PF 07-OCT-1999; 99WO-US023519.
XX XX
PR 07-OCT-1998; 98US-0103322P.
PR 30-OCT-1998; 98US-0106473P.
PR 23-DEC-1998; 98US-0114088P.
XX XX
PA (WARN ) WARNER LAMBERT CO.
XX XX
PI Johns MA, Moldover B, Offord JD;
XX XX
DR WPI; 2000-303744/26.
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DR P-PSDB; AAY92321.
XX
PT New human nucleic acids encoding the alpha2delta-C and alpha2delta-D
PT proteins, useful in the treatment of epilepsy, migraine, chronic pain,
PT anxiety, multiple sclerosis or cancer.
XX
PS
XX Claim 1; Page 64-66; 88pp; English.
XX
CC The alpha-2-delta-D gene encodes a calcium channel subunit polypeptide.
CC The gene has been mapped to chromosome 12p13.1. This gene and the related
CC alpha-2-delta-C and -B genes are useful for protecting mammalian cells
CC from abnormal calcium flux by introducing expression vectors containing
CC the respective gene into mammalian cells. The antisense genes are also
CC useful for treating or preventing epilepsy. The alpha-delta-2-A protein
CC is a high-affinity binding target of the anti-convulsant drug gabapentin.
CC Therefore, alpha-delta-2 proteins may also be targeted to treat seizure-
CC related syndromes, migraine, ataxia, vestibular defects, chronic pain,
CC sleep interference, anxiety, amyotrophic lateral sclerosis (ALS), multiple
CC sclerosis, mania, tremor, parkinsonism, substance abuse or addiction
CC syndromes, mood, depression or cancer
XX
SQ Sequence 5073 BP; 1280 A; 1390 C; 1347 G; 1056 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0 Length: 5073
Score: 5386.50 Matches: 1035
Percent Similarity: 97.47% Conservative: 4
Best Local Similarity: 97.09% Mismatches: 27
Query Match: 94.07% Indels: 1
DB: 3 Gaps: 0
US-09-833-222A-10 (1-1090) x AAA09254 (1-5073)
QY 11 AspArgValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLys 30
DB : : :
DB 174 GAAACAGTGAAGCTATGGGTGCACACCTTCGGGGGACCTGTATACACTGTGACCAA 233
QY 31 TyrSerGlySerLeuLeuGlnLysLysLysLysLysLysLysLysLysLysLysLys 50
DB TACTCAGGCTCTCTCTTGTCTGCAAGAGTACAGGATGTGGATCTGAGTCTGAAGATC 293
QY 51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu 70
DB GAGGAGGTGGATGGCTTGGAGCTGGTGAGGAGTCTCTCAGAGACATGGAGAACATGCTG 353
QY 71 ArgArgLysValGluAlaValGlnAsnLeuValGluAlaGluAlaGluAlaAspLeuAsn 90
DB CGAGAGGAAGTCGAGGCGGTCCAGAAATCTGTGGAAGCTGCCGAGGAGGCGCCACCTGAAC 413
QY 91 HisGluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuLysLysLysLys 110
DB CACGAATTCGAATGAAATCCCTGGTGTTCGATTTACACTCGGTCTCTGATCAACAGAGAG 473
QY 111 AspGluLysGlyAsnPheValGluLeuGlyValaGluPheLeuLeuGluSerAsnAlaHis 130
DB GACGAGAGGGCAACTTCGTGGAGCTGGGGCGCCGAGTTCTCTGGAGTCCAATGTCTCAC 533
QY 131 PheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyr 150
DB TTCAGCAACCTGCGGTGGAACCTCCATCAGCAGCGTGCAGTGGCCCAACACGCTGTAC 593
QY 151 AsnLysAspProAspLeuLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPhe 170
DB AACAAAGACCCAGATATTTTAATGGAGTCTACATGCTCGAAGCCTTGAATGCTGTCTTC 653
QY 171 ValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGly 190
DB GTGGAGAACTTCCAGAGAGACCCAAACGTTGACCTGGCAATATTTTGGCAGTGCACCTGGA 713
QY 191 PhePheArgIleTyrProGlyLysLysLysLysLysLysLysLysLysLysLysLys 210
DB TTCTTCAGGATCTATCAGGTATAAAATGGACACCTGATGAGAAATGGAGTCTTACTTTT 773

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1854 Db GACTACTTCTTACGGACATCAGCACCCCTTTTCAGTTTGGGGGTGCTGCTGTCGCGG 1913
591 Qy GlyHisGlyGluTyrIleLeuLeuGlyAenThrSerValGluGluGlyLeuHisAspLeu 610
1914 Db GGCACAGGAATACATCTTCTGGGGAACAGCTGTGGGAAGAAGGCTGCATGACTTG 1973
611 Qy LeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspPro 630
1974 Db CTTCAACCAGACCTGGCCCTGGCCGTGACTGGATCTACTGCATCACAGATATTGACCCA 2033
631 Qy AspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspPro 650
2034 Db GACCAACCGAAGCTCAGCAGCTAGAGCCATGATCCGCTTCCACAGGAAGACCCA 2093
651 Qy AspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAlaValIleThrAla 670
2094 Db GACCTGGAGTGTGACGAGAGCTGCTCGCGAGGTGCTGTTTGACGCGGTGTCACAGCC 2153
671 Qy ProMetGluAlaTyrThrAlaLeuAlaLeuLeuMetSerGluGluSerGluHisVal 690
2154 Db CCCATGGAAGCTTACTTGACACGCTGGCCCTCAACATGTCGAGGAGTCTGAACACGTTG 2213
691 Qy ValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGly 710
2214 Db GTGACATGGCCCTTCTGGGCACCCGGGCTGGCCCTCCTGGAAGCAGCTTGTTCGTGGGC 2273
711 Qy SerGluLysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThr 730
2274 Db TCCGAGAAGTCTCCGACAGGAAGTCTCTGACACTGAGGACGAGGCCAGCGTGTTCACC 2333
731 Qy LeuAspArgPheProLeuTyrTrpArgGlnAlaSerGluHisProAlaGlySerPheVal 750
2334 Db CTGACCGCTTCCCGCTGTGTGTACCGCAGGCTCAGAGCATCTGCTGGCAGCTTCGTC 2393
751 Qy PheLeuLeuArgTTPAlaGluGlyProGluSerAlaGlyLeuProMetValValThrAla 770
2394 Db TTCAACCTCCGCTGGGAGAGGACAGAAAGTGGGGTGAACTGAGTGGTGGTACGGCA 2453
771 Qy SerThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAlaAlaGlyVal 790
2454 Db AGCACAGCTGGCGGTGACCGTGCACAGAGGACAGCCATTGCTGCAGCGCGGGGCTC 2513
791 Qy GlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaIleThrArgGlnCysSerThr 810
2514 Db CAAATGAAGCTGGAATCTCTCAGCGCAAAATCTGGGCGGCAACGCGCAGTGCGACCT 2573
811 Qy ValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAsp 830
2574 Db GTGATGGGCGTGCACACAGAGCTGCGAGGACAGTATCTGGACTGCTTCGTTCATCGAC 2633
831 Qy AsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGlu 850
2634 Db AACAAAGGTTCATCTGATCTCCAGAGGTCCCGAGAGAGCGGAAGATTTCTGGGGGAG 2693
851 Qy ValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMet 870
2694 Db GTGATGGTGTGTCCTGACCCAGCTGCTCAGCATGGGGGTGTTTCAGCCCAAGTGACTATG 2753
871 Qy TyrAspTyrGlnAlaMetCysLysProSerSerHisHisSerAlaAlaGlnProLeu 890
2754 Db TATGACTATCAGGCCATGTGCAAAACCTTCAGAGTCACCCACAGTGCAGGCCAGCCCTG 2813
891 Qy ValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnLeuValLeu 910
2814 Db GTACGCCCAATTTCTGCTTCTTACCGCGCACAGGTGGCTGCTGCAGAGGAGCTGGTCTG 2873
911 Qy PheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSer 930
2874 Db TTCTGTGTGAGTGGAGTGTCTGGGGCTCTCTGGTACGACAGAGGGGCGGAGGCCAAAGT 2933
931 Qy ValPheHisHisSerHisLysHisLysGlnAspProLeuGlnProCysAspThrGlu 950

2934 Db GTCTTCCATCAGTCCCAACAACAAGACAGACCCGCTGCGACCCCTCGACACGGAG 2993
951 Qy TyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGly 970
2994 Db TACCCCGTGTTCGTATACAGCGCGCCATCCGGAGGCCAACGGGATCTGGAGTGGGG 3053
971 Qy ProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLeuLeuVal 990
3054 Db CCCTGCCAGAGGTATTGTGTGTGCAGCATTTCCCAACAGTAACTCTCTCTCTGCTG 3113
991 Qy ThrAspProThrCysAspCysSerIlePheProProValLeuGlnGluAlaThrGluVal 1010
3114 Db ACAGACCCCACTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3173
1011 Qy LysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeuLeuArgArgPro 1030
3174 Db AATATAATGCTCTGTCAAAATGTACCGGATGCGCTCCAGAGCTCCCGCGCGACCA 3233
1031 Qy AspSerCysHisAlaPheHisProGluValArgValGluAlaAspArgGlyTrpAlaGly 1050
3234 Db GACTCTGCCACGCTTCCATCCAGAGGAGAAATGCCAGGACTGCCGCGCGCTCGGAC 3293
1051 Qy PheSerSerProAsnProLeuCysLeuGlyLeuCysProCysArgGlnGluHisIleGly 1070
3294 Db ACCTCAGCTCGCGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3352
1071 Qy MetProMetAsnThrPro 1076
3353 Db ACTCCTCGGTGACACCA 3370
RESULT 4
ADE07110
ID ADE07110 standard; DNA; 4841 BP.
XX
AC ADE07110;
XX
DT 29-JAN-2004 (first entry)
XX
DE Novel coding sequence (useful for identifying genetic disorders) #176.
XX
KW novel gene; novel protein; tissue marker; molecular weight marker;
KW chromosome marker; genetic disorder; gene; ds.
XX
OS Unidentified.
XX
PN WO2003054152-A2.
XX
PD 03-JUL-2003.
XX
PF 10-DEC-2002; 2002WO-US039555.
XX
PR 10-DEC-2001; 2001US-0339739P.
PR 11-DEC-2001; 2001US-0339453P.
PR 14-MAR-2002; 2002US-0365091P.
PR 14-MAR-2002; 2002US-0365384P.
PR 12-APR-2002; 2002US-0372381P.
PR 12-APR-2002; 2002US-0372615P.
PR 22-APR-2002; 2002US-00128558.
PR 24-APR-2002; 2002US-0376045P.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;
PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
XX
DR WPI; 2003-569235/53.
DR P-PSDB; ADE08021.
XX
PT New polynucleotides, useful for expressing recombinant proteins for
PT analysis, characterization or therapeutic use, or as markers for tissues
PT in which the corresponding protein is preferentially expressed.
XX

PS Claim 1; SEQ ID NO 176; 1177pp; English.

XX The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: CC markers for tissues in which the corresponding protein is preferentially CC expressed; as molecular weight markers on gels; as chromosome markers or CC tags; to identify chromosomes or to map related gene positions; and to CC compare with endogenous DNA sequences in patients to identify potential CC genetic disorders. The present DNA sequence represents a gene of the CC invention.

XX

SQ Sequence 4841 BP; 1176 A; 1335 C; 1339 G; 991 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	4841
Score:	5385.50	Matches:	1034
Percent Similarity:	97.47%	Conservative:	5
Best Local Similarity:	97.00%	Mismatches:	27
Query Match:	94.05%	Indels:	1
DB:	10	Gaps:	0

US-09-833-222A-10 (1-1090) x ADE07110 (1-4841)

QY 11 AspArgValIysLeuTrpAlaAspThrPheGlyAspLeuTyrAenThrValThrLys 30
::

Db 498 GAAACAGTGAAGCTATGGGCTGACACCTTCGGCGGGACCTGTATACACTGTGACCAA 557

QY 31 TyrSerGlySerLeuLeuLeuGlnLysLysTyriysAspValGluSerSerLeuLysIle 50

Db 558 TACTCAGGCTCTCTCTGGCTGCGAGAGAACTACAAAGATGTGGATCCAGTCTGAAGATC 617

QY 51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAenMetLeu 70

Db 618 GAGAGGTGATGGCTTGGAGCTGGTGAGGAGTTCTCAGAGACATGGAGAACATGCTG 677

QY 71 ArgArgLysValGluAlaValGlnAsnLeuValGluAlaGluAlaGluAlaAspLeuAsn 90

Db 678 CGGAGGAAATCGAGGCGGTCAGAAATCTGGTGAAGCTGCCGAGGAGCGCACCTGAAAC 737

QY 91 HisGluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArg 110

Db 738 CACGAATTCGAATGAATCCCTGGGTTCGACTATATACAACTCGGTCCTGTATCAACGAGAG 797

QY 111 AspGluLysGlyAsnPheValGluLeuGlyValGluPheLeuLeuGluSerAsnAlaHis 130

Db 798 GACGAGNAGGGCAACTTCGTGGAGCTGGGCGCGAGTTCTCTCGAGTCCATATGCTCAC 857

QY 131 PheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyr 150

Db 858 TTCAGCAACTGCGCGGTGAACCTCCATCAGCAGCGGTGAGCTGCCACCAACGTGTAC 917

QY 151 AsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPhe 170

Db 918 AACAAAGACCAGATATTTTAAATGGAGTGTACATGTCTGAAGCCTTGAATGTCTTTC 977

QY 171 ValGluAsnPheGlnArgAspProThrLeuThrTyrGlnTyrPheGlySerAlaThrGly 190

Db 978 GTGGAGNACTTCAGAGAGACCAACGTTGACTGGCAATATTTTGGCAGTGCACCTGGA 1037

QY 191 PhePheArgIleTyrProGlyIleLysTyrThrProAspGluAsnGlyValIleThrPhe 210

Db 1038 TTCTTCAGGATCTATCCAGGTATATAAATGGACACCTGATGAGAATGGAGTCACTTTT 1097

QY 211 AspCysArgAsnArgGlyTyrTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIle 230

Db 1098 GACTGCGGAAACCGCGCTGTATCATTTCAAGCTGTACTTCTCCCAAGGACATAGTGATT 1157

QY 231 LeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIle 250

Db 1158 TTGGTGGACGTGAGCGGCACTATGAGGGGCTGAGGATGATGATTTGCCAAGCACCAATC 1217

QY 251 ThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAsp 270
:::

Db 1218 ACCACCATCTTGGACACACCCCTGGGGGAGAATGACTTCAATTAATATCATAGCTCAATGAC 1277

QY 271 TyrValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsn 290
|||||

Db 1278 TAGCTCCATTACATCAGAGCTTGTTTAAAGGGATCTCTGTCAGGCGGACCCAGACAAT 1337
|||||

QY 291 ArgGluHisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAsp 310
|||||

Db 1338 CGAGAGCATTTCAAACCTGCTGGTGGAGGAGTTGATGGTCAAAGGTGTGGGGGTCTGGAC 1397
|||||

QY 311 GlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySer 330
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Db 1398 CRAAGCCTTGAGAGAGCCTTCCAGATCTCGAAGCAGTTCCAGAGAGCCCAAGCAAGGAAGC 1457
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QY 331 LeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProVal 350
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Db 1458 CTCTCAACACAGGCCATCATGCTCATCAGCAGCGCGCGTGGAGGACTACAGAGCCGGTG 1517
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QY 351 PheGluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArg 370
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Db 1518 TTTGAGAAGTATAACTGGCCAGACTGTAAAGTCCGAGTTTTCATTACCTCATTTGGGAGA 1577
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QY 371 GluValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThr 390
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Db 1578 GAAGTGTCTTTGCTCAGCGCATGAAGTGGATTGTCATGCAACCAACAAAGGCTACTACACG 1637
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QY 391 GlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSer 410
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Db 1638 CAGATCTCAACCGCTGGCGGACACCCAGAGAGAACGTGATGGAATACCTGACAGTGTCTCAGC 1697
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QY 411 ArgProMetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSer 430
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Db 1698 CGCCCCATGGTCACTCAACCAACGACACGACATCATCTGGACAGAGCCCTACATGGACAGC 1757
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QY 431 LysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuThrThrValAlaMetProVal 450
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Db 1758 AAGCTCTCAGCTCGCAGGCTCAGAGCCTGACACTGTCACCACTGTGGCATGGCCAGTC 1817
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QY 451 PheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp 470
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Db 1818 TTCAGCAAGAAGAACCAACCGCATCCCATGGCATTTCTCTGGGTGTGGTGGCTTCAGAT 1877
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QY 471 ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyr 490
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Db 1878 GTGGCCCTGAGAGAGCTGATGAAGCTGGCGCCCGGTACAAGCTTGGAGTGACCGGATAC 1937
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QY 491 AlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr 510
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Db 1938 GCCTTTCTGAAACACCAACAATGGCTACATCTCTCCCATCCCGACCTCCGCGCCCTGTAC 1997
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QY 511 ArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluVal 530
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Db 1998 AGAGGGGGAAGAACTAAACCCAAACCTTAACCTCAACAGTGGATCTCTCCGAAGTG 2057
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QY 531 GluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr 550
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Db 2058 GAGTGGAGAGACCGGCTGAATCTCTGAGACAGCCATGATCAATAGGGAACAGGTACT 2117
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QY 551 LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn 570
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Db 2118 CTCTCATGGATGTGAAGGTTCGATGGATAAAGGAAGCGAGTTCTTTTCTTGACCAAT 2177
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QY 571 AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg 590
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Db 2178 GACTACTCTTTCACGGACATCAGCAGACCCCTTTTCAGTTTGGGGGTGGTGTCTCCCGG 2237
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QY 591 GlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeu 610
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Db 2238 GGCCACGGAGAATACATCTCTTGGGGAAACAGCTCTGTGGAAAGAGCCCTGCATGACTTG 2297
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QY 611 LeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspPro 630
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Db 2298 CTTACCCAGACCTGGCCCTGGCCGCTGACTGATCTACTGTCATCAGATATTGACCCA 2357
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Qy 631 AspHisArgTysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspPro 650
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Qy 651 AspleuGluCysAspGluLeuValArgGluValLeuPheAspAlaValValThrAla 670
Db GACCTGAGTGTGACGAGGAGCTGGTCCGGAGAGTGTCTTTGACCGGGTGTGACAGCC 2477
Qy 671 ProMetGluAlaTyrTrpThrAlaLeuAlaLeuAenMetSerGluGluSerGluHisVal 690
Db CCCATGGAAGCTTACTGGACAGCGCTGGCCCTCAACATGTCCGAGGAGTCTGAACAGTG 2537
Qy 691 ValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGly 710
Db GTGGACATGGCTTCTTGGGACCCCGGCTGGCCCTCTCTGAGAAGCAGCTTGTTCGTGGGC 2597
Qy 711 SerGluLysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThr 730
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Qy 731 LeuAspArgPheProLeuTyrTrpArgGlnAlaSerGluHisProAlaGlySerPheVal 750
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Qy 751 PheAenLeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAla 770
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Qy 771 SerThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAlaAlaGlyVal 790
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Qy 831 AsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGlu 850
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Qy 851 ValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMet 870
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Qy 871 TyrAspTyrGlnAlaMetCysLysProSerSerHisHisSerAlaAlaGlnProLeu 890
Db TATGACTATCAGGCCATGTGCAAAACCTTCGAGTCACCAACACAGTCGAGCCCGCCCTG 3137
Qy 891 ValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnLeuValLeu 910
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Qy 911 PheLeuLeuGluTyrSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSer 930
Db TTCTGTCTGGAGTGGAGTGTCTGGGGCTCTCTGTGTACACAGAGGGGGCGGACCAAGT 3257
Qy 931 ValPheHisHisSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGlu 950
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Qy 971 ProCysGlnLysValPheValValGlnGlnIleProAenSerAenLeuLeuLeuVal 990
Db CCCTGCCAGAAAGTATTGTTGGTGCAGCAGATTCCCAACAGTAACCTTCTCTCTCTGTTG 3437

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Qy 1031 AspSerCysHisAlaPheHisProGluValArgValGluAlaAenArgArgGlyTrpAlaGly 1050
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Qy 1051 PheSerSerProAenProLeuCysLeuGlyLeuCysProCysArgGlnGluHisIleGly 1070
Db ACCTCAGCTCGCGCGCTTCTCTGCT-GCCTGTGTGTGCTGCTGGGGGTACTGCCCCA 3676
Qy 1071 MetProMetAenThrPro 1076
Db ACTCTCGCGGTGACACCA 3694
RESULT 5
AAS01433
ID AAS01433 standard; cDNA; 3339 BP.
XX AAS01433;
AC AAS01433;
XX 04-JUL-2001 (first entry)
DT Human secreted soluble alpha2delta calcium channel subunit #18 cDNA.
XX Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;
XX alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;
XX gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;
XX filter binding assay; wheat germ lectin flashplate assay; ss.
OS Homo sapiens.
XX Key Location/Qualifiers
FT CDS 3..3339
FT /tag= a
FT /partial
FT /product= "Alpha2delta calcium channel subunit #18"
FT /note= "This sequence lacks a stop codon"
FT /transl_except= (pos:2241..2246,aa:Ala-Ser-Gly)
FT /note= "These codons have an apparent 3 nucleotide
FT deletion"
FT /transl_except= (pos:2286..2340,aa:Ser-Asp)
FT /note= "These two codons between them have an apparent 49
FT nucleotide insertion which alters the reading frame"
XX WO200119870-A2.
PN 22-MAR-2001.
PD 18-SEP-2000; 2000WO-EP009137.
PF 16-SEP-1999; 99US-00397550.
PR (WARN) WARNER LAMBERT CO.
PA Brown JP, Bertelli F;
XX WPI; 2001-235262/24.
DR P-PSDB; AAU01038.
XX Calcium channel alpha2delta subunits, useful in e.g. SPA assays,
PT Flashplate assays, Nickel Flashplate assays, Filter binding assays or
PT Wheat Germ Lectin Flashplate assays.
XX Claim 39; Page 148-149; 160pp; English.
PS The present sequence encodes for human secreted calcium channel
CC alpha2delta subunit #18 which is soluble and retaining the functional

CC characteristics of the full length or wild type alpha2delta subunit
 CC (AAU01025) from which it is derived. The invention relates to truncated
 CC alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins
 CC which retain their affinity for radioactively labelled gabapentin. The
 CC alpha2delta subunit is 1 of the components of the heteromultimeric
 CC voltage-dependent calcium channel (VDCC) complexes present in neuronal
 CC and non-neuronal tissues including heart and skeletal muscle. Numerous
 CC soluble forms of the human calcium channel alpha2delta subunits (AAU01014
 CC -AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the porcine
 CC calcium channel alpha2delta subunits (AAU01027-AAU01031) are described.
 CC The secreted soluble alpha2delta subunit may be used in assays e.g.
 CC scintillation proximity assay (SPA), flashplate, nickel flashplate,
 CC filter binding or wheat germ lectin flashplate assays to detect or
 CC measure the binding or interaction of a ligand (e.g. gabapentin, L-
 CC Norleucine, L-Allo-Isoleucine, L-methionine, L-Leucine, L-Isoleucine, L-
 CC Valine, Spermine and/or L-Phenylalanine) of a calcium channel alpha2delta
 CC subunit
 XX

SQ Sequence 3339 BP; 780 A; 934 C; 960 G; 665 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 3339
 Score: 5342.50 Matches: 1028
 Percent Similarity: 97.54% Conservatives: 2
 Best Local Similarity: 97.35% Mismatches: 8
 Query Match: 93.30% Indels: 18
 DB: 4 Gaps: 2

US-09-833-222A-10 (1-1090) x AAS01433 (1-3339)

QY 11 AspArgValLysLeuTrpAlaAspThrPheGlyAspLeuTyrAsnThrValThrLys 30
 DB : : :
 DB 174 GAAACAGTGAAGCTATGGCTGACACCTTCGGCGGGGACCTGTATACACTGTGACCAA 233
 QY 31 TyrSerGlySerLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIle 50
 DB TACTCAGGCTCTCTCTTGTCTGCAAGAAGTACAAGGATGTGGATCTCGAAGATC 293
 QY 51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu 70
 DB GAGGAGTGGATGGCTTGGAGCTGGTGGAGAGTTCTCAGGAGCATGGAGAACATGCTG 353
 QY 71 ArgArgLysValGluAlaValGlnAsnLeuValGluAlaGluAlaGluAlaAspLeuAsn 90
 DB CGGAGGAAAGCTCGAGGCGGTCAGAAATCTGCTGGAAGCTGCCGAGGAGCGGACCTG 413
 QY 91 HisGluPheAsnGlnSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArg 110
 DB CACGAATTCATGAATCCCTGGTGTTCGACTATTACAACCTCGGTCCTGATCAACGAG 473
 QY 111 AspGluLysGlyAsnPheValGluLeuGlyValGluPheLeuLeuGluSerAsnAlaHis 130
 DB GACGAGNAGGGCAACTTCGTGGAGCTGGGCGCCGAGTTCTCTCGAGTCCAATGCTCAC 533
 QY 131 PheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyr 150
 DB TTCAGCAACCTGCGCGGTGAACCTCCATCAGCAGCGTGCGAGTGCACCAACGCGTAC 593
 QY 151 AsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPhe 170
 DB AACAAAGACCCAGATATTTTAAATGGAGTCTACATGCTGGAAGCCCTTGAATGCTGCTTC 653
 QY 171 ValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGly 190
 DB GTGGAGAACTTCCAGAGAGCCCAACGTTGACCTGGCAATATTTTGGCAGTGCNACTGGA 713
 QY 191 PhePheArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPhe 210
 DB TTCTTCAGGATCTATCCAGGTAATAAATGGACACCTGATGAGAATGGAGTCACTACTTT 773
 QY 211 AspCysArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIle 230
 DB GACTTCGCGAAACCGCGGCTGGTACATTCAAGCTGCTACTTCTCCCAAGGACATAGTGATT 833

QY 231 LeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIle 250
 DB TTGGTGGAGCTGAGCGGCGAGTATGAAGGGGCTGAGGATGACTATTCGCAAGACACCATC 893
 QY 251 ThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAsp 270
 DB ACCACCATCTTGGACACCCCTGGGGGAGATGACTTCGTTAATATCATAGGCTCAATGAC 953
 QY 271 TyrValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsn 290
 DB TACGTCATTTACATCGAGCCTGTTTAAAGGGATCCTCGTCCAGGCGGACCGAGACAAT 1013
 QY 291 ArgGluHisPheLysLeuValGluLeuMetValLysGlyValGlyValValAsp 310
 DB CGAGAGCATTTCAACTCTGTGTGGAGGAGTTGATGCTCAAGGTGTGGGGGTCTGGAC 1073
 QY 311 GlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySer 330
 DB CAAAGCCTCGAGAGAGCCCTTCCAGATCTCGAGCAGTTCCAGAGGCGCAAGGAAGC 1133
 QY 331 LeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProVal 350
 DB CTCTGCAACACGAGGCCATCATGCTCATCAGCGACGCGCGCTGGAGGACTACGAGCGCGTG 1193
 QY 351 PheGluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArg 370
 DB TTTGAGAGATTAACCTGGCCAGACTGTAAAGTCCGAGTTTTCTACTTACCTCATTTGGAGA 1253
 QY 371 GluValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThr 390
 DB GAAGTGCTTTTGTGACCGCATGAAGTGGATTGTCATGCAACAACAAGGCTACTACACG 1313
 QY 391 GlnIleSerThrIleuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSer 410
 DB CAGATCTCAACGCTGGCGGACACCCAGGAGAAAGCTGATGAGAAATACCTGCAGCTGCTCAGC 1373
 QY 411 ArgProMetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSer 430
 DB CGCCCCATGGTTCATCAACCAACCAACGACATCATCTGGACAGAGGCTTACATGGACAGC 1433
 QY 431 LysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProVal 450
 DB AAGCTCTCAGCTCGCAGGCTCAGAGCTGACACCTGCTCACCACCTGTGCCATGCCAGTC 1493
 QY 451 PheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp 470
 DB TTCAGCAAGAGAACGAAACGCGCATCCCATGGCATTTCTCTGGGTGTGGTGGCTCAGAT 1553
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 DB GTGGCCCTGAGAGAGCTGATGAAGTGGGCGCCCGGTACACAGCTTGGAGTGCACGATAC 1613
 QY 491 AlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr 510
 DB GCCTTTCTGAACACCAACAATGGCTACATCTCTCCATCTCCGACCTCCGCCCCCTGTAC 1673
 QY 511 ArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluVal 530
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 QY 531 GluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr 550
 DB GAGTGGAGAGACGAGCTGNAATCTCTGAGAACAGCCATGATCAATAGGAGAAACAGGTACT 1793
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 DB GACTACTTCTTCCAGCAGACATCAGCAGACCCCTTTTCAAGTGTGGGTGGTGTGCTGCCGG 1913

Qy 591 GlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeu 610
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Qy 611 LeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspPro 630
Db 1974 CTTCAACCAGACCTGGCGCCCTGGCGGTGACTGGATCTACTGCATCACAGATATTGACCCA 2033
Qy 631 AspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspPro 650
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Qy 651 AspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAlaValThrAla 670
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Qy 701 -----GlyLeuLeuArgSerSerLeuPheValGlySerGluLysVa 714
Db 2274 TCCGAGAAGGTCTCCGAGTGGCCCTCTCAGAGCAGCTTGTTCGTGGGCTCCGAGAAGGT 2333
Qy 714 lSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThrLeuAspArgPh 734
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Qy 734 eProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheValPheAsnLeuAr 754
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Qy 774 lAlaValThrValAspLysArgThrAlaIleAlaAlaAlaGlyValGlnMetLysLe 794
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Db 3114 GGTATTGTTGGTGAGCAGATTCACACAGTAACTCTCTCTCTGGTGCAGACCCAC 3173
Qy 994 rCysAspCysSerIlePheProValLeuGlnGluAlaThrGluValLysTyrAsnAl 1014
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Db 3234 CTCTGTCAATGTGACCGGATCGCTCCAGAGCTCCGCGGCGGACAGACTCTTGCCA 3293
Qy 1034 sAlaPheHisProGluValArgValGluAlaAspArgGlyTrpAla 1049
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RESULT 6
AAFS7570
ID AAFS7570 standard; DNA; 3339 BP.
XX
AC AAFS7570;
XX
DT 11-JUN-2001 (first entry)
XX
DE Human calcium channel alpha2delta subunit encoding DNA.
XX
KW Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;
KW nervous system disorder; pain; epilepsy; anxiety; human; ds.
XX
OS Homo sapiens.
XX
PN WO200120336-A2.
XX
PD 22-MAR-2001.
XX
PF 18-SEP-2000; 2000WO-EP009136.
XX
PR 16-SEP-1999; 99US-00397549.
XX
PA (WARN) WARNER LAMBERT CO.
XX
PI Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;
XX
DR WPI; 2001-257902/26.
XX
CC Competitive binding assay for screening ligands which bind a cerebral
cortical voltage-dependent calcium channel alpha2-delta-1 subunit, where
the ligands identified are useful for treating disorders of the nervous
system, including pain.
XX
PS Disclosure; Page 146-147; 158pp; English.
XX
CC The invention relates to a new method for screening ligands which bind a
cerebral cortical voltage-dependent calcium channel alpha2delta subunit,
preferably alpha2delta-1 subunit. The method comprises contacting a
secreted soluble recombinant alpha2delta-1 subunit with a ligand of
interest and a labelled compound which binds the subunit, followed by
measuring the level of binding of the labelled compound to alpha2delta-1
subunit. The method is useful for screening ligands, preferably
biologically active products that modulate a nervous system function,
which bind a cerebral cortical voltage-dependent calcium channel
alpha2delta-1 subunit. The ligands identified by the method are useful
for treating disorders of the nervous system, including pain, epilepsy
and anxiety. The present sequence represents a human calcium channel
alpha2delta subunit encoding DNA
XX

SQ	Sequence	3339 BP; 780 A; 934 C; 960 G; 665 T; 0 U; 0 Other;
Alignment Scores:		
Pred. No.:	0	Length: 3339
Score:	5342.50	Matches: 1028
Percent Similarity:	97.54%	Conservative: 2
Best Local Similarity:	97.35%	Mismatches: 8
Query Match:	93.30%	Indels: 18
DB:	5	Gaps: 2
US-09-833-222A-10 (1-1090) x AAF57570 (1-3339)		
Qy	11	AspArgValLysLeuTrpAlaAspThrPheGlyAspLeuTyrrAsnThrValThrLys 30
Db	174	GAACAGTGAAGCTATGGCTGACACCTTCGGCGGGACCTGTATAACACTGTGACCAA 233
Qy	31	TyrSerGlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIle 50
Db	234	TACTCAGGCTCTCTTGTCTGCAGAGAAGTACAAAGATGTGGAGTCCAGTCTGAAAGATC 293
Qy	51	GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu 70
Db	294	GAGAGGTGGTGGCTTGGAGCTGGTGGAGAGTTCTCAGAGCATGGAGACATGCTG 353
Qy	71	ArgArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsn 90
Db	354	CGGAGGAAAGTCGAGGCGGTCAGAAATCTGTGGAAGCTGCCGAGGAGCGGACCTGAAC 413
Qy	91	HisGluPheAsnGluSerLeuValPheAspTyrTrpAsnSerValLeuIleAsnGluArg 110
Db	414	CACGAATTCGAATGAATCCCTGGTGTTCGACTATTACAACTCGGTCTTGATCAACGAGAG 473
Qy	111	AspGluLysGlyAsnPheValGluLeuGlyValaGluPheLeuLeuGluSerAsnAlaHis 130
Db	474	GACGAGAAGGCAACTTCGTGGAGCTGGGCGCCGAGTTCCTCTGGAGTCCAATGCTCAC 533
Qy	131	PheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyr 150
Db	534	TTCAGCAACCTGCCGGTGAACACCTCCATCAGCAGCGTGCAGCTGCCACCAACGCTGAC 593
Qy	151	AsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPhe 170
Db	594	AACAAAGACCCAGATATTTAAATGGAGTCTACATGCTCGAAGCTTGAATGCTGCTTC 653
Qy	171	ValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGly 190
Db	654	GTGGAGAACTTCGAGAGACCCACGTTGACCTGGCAATATTTGGCAGTGCACATGGA 713
Qy	191	PhePheArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPhe 210
Db	714	TTCTTCAGGATCTATCCAGGTATAAATGGACACCTGATGAGAATGGAGTCAATTACTTTT 773
Qy	211	AspCysArgAsnArgGlyTrpTyrIleGlnAlaThrSerProLysAspIleValIle 230
Db	774	GACTGCCGAACCCGCGCTGGTACATTCAGAGCTGCTACTCTCCCAAGGACATAGTGATT 833
Qy	231	LeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIle 250
Db	834	TTGGTGGACGTGAGCGCATGTGAAGGGCTGAGGATGACTATTGCCAAGCACCAATC 893
Qy	251	ThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAsp 270
Db	894	ACCACCATCTTGACACCCCTGGGGAGAAATGACTTCGTTAATATCATAGCGTACAATGAC 953
Qy	271	TyrValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsn 290
Db	954	TACGTCCATTACATCGAGCTTGTTTTAAAGGATCCCTCGTCAGCGCGGACCGAGACAAT 1013
Qy	291	ArgGluHisPheLysLeuLeuValGluLeuMetValLysGlyValGlyValValAsp 310
Db	1014	CGAGAGCATTTCAAATCTGCTGGTGGAGAGTTGATGGTCAAAAGTGTGGGGGTCTGGAC 1073
Qy	311	GlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySer 330
Db	1074	CAAGCCTCAGAGAAAGCCTTCCAGATCCTCAAGCAGTTCTCAAGAGGCCAAGCAAGGAAGC 1133
Qy	331	LeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProVal 350
Db	1134	CTCTGCAACACAGGCCATCATGTCTCAGCGAGCGCGCGTGGAGACTACAGAGCCGGTG 1193
Qy	351	PheGluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArg 370
Db	1194	TTTGAGAGTATTAACCTGGCCAGACTGTAAAGTCCGAGTTTTCATTACCTCATTTGGAGA 1253
Qy	371	GluValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThr 390
Db	1254	GAAGTGTCTTTTCTCAGCCGATGAAGTGGATTGCATGCAACAACAAGAGGCTACTACACG 1313
Qy	391	GlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSer 410
Db	1314	CAGATCTCAACGCTGGCGGACACCCAGGAGAACGTATGGAATACCTGCACGCTCAGC 1373
Qy	411	ArgProMetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSer 430
Db	1374	CGCCCCATGGTCAATCAACCGACACGACATCATCTGGACAGAGGCTACATGGACAGC 1433
Qy	431	LysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrValAlaMetProVal 450
Db	1434	AGCTCCTCAGCTCGCAGGCTCAGAGCCTGACACTGTCACCACTGTGGCCATGCCAGTC 1493
Qy	451	PheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp 470
Db	1494	TTCAGCAAGAAAGAACCAACCGCATCCCATGGCATTTCTCTGGGTGTGGTGGCTCAGAT 1553
Qy	471	ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyr 490
Db	1554	GTGGCCTCAGAGAGCTGATGAAGCTGGCGCCCCGGTACAAGCTTGGAGTGCACGGATAC 1613
Qy	491	AlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr 510
Db	1614	GCCTTTCTGAACACCAACCAATGGCTACATCTCTCCCATCCCGACCTCGGCCCTGTAC 1673
Qy	511	ArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluVal 530
Db	1674	AGAGGGGGAAGAACTAAACCCAAACCTAACTACAAACAGTGTGGATCTCTCCGAAGTG 1733
Qy	531	GluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr 550
Db	1734	GAGTGGAGAACCGAGCTGAATCTCTGAGAACAGCCATCATCAATAGGGAACAGGTACT 1793
Qy	551	LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn 570
Db	1794	CTCTCGATGGATGTGAAGGTTCCGATGGATAAAGGAAGCGAGTTCTTTTCTGTGACCAAT 1853
Qy	571	AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg 590
Db	1854	GACTACTCTTTCAGCGACATCAGCGACACCCCTTTTCAGTTTGGGGGTGTGTGTCCTCCGG 1913
Qy	591	GlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeu 610
Db	1914	GGCCACGGAGATACATCTCTTGGGGAACACGCTGTGTGGAAGAGCCCTGCATGACTTC 1973
Qy	611	LeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspPro 630
Db	1974	CTTCAACCCAGACCTGGCCCTGGCCGGTACTGGATCTACTGCAATCACAGATATTGACCCA 2033
Qy	631	AspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspPro 650
Db	2034	GACCCCGGAAGCTCAGCAGCTAGAGGCCATGATCCGCTTCTCTACCCAGGAAGGACCCA 2093
Qy	651	AspLeuGluCysAspGluLeuValArgGluValLeuPheAspAlaValValThrAla 670
Db	2094	GACCTGGAGTGTGACGAGGAGCTGGTCCGGGAGGTGCTGTTTTCACGCGGTGGTGACGCC 2153
Qy	671	ProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisVal 690

Db 2154 CCCATGGAAGCCTACTGTGACACAGCCCTGGCCCTCAACATGTCCGAGGAGTCTGAAACAGTG 2213
Qy 691 ValAspMetAlaPheLeuGlyThrArgAla----- 700
Db 2214 GTGGACATGGCTTCTCTGGGCACCCGGGCTGGCCCTCTCTGAGAACGAGCTTGTTCGTGGGC 2273
Qy 701 -----GlyLeuLeuAtrgSerSerLeuPheValGlySerGluLysVa 714
Db 2274 TCCGAGAAGGTCTCCGAGTGGCCCTCTGAGAAGCAGCTTGTTCGTGGGCCTCCGAGAAGGT 2333
Qy 714 lSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThrLeuAspArgPh 734
Db 2334 CTCCGACAGGAAGTCTCTGACACCTGAGGACGAGCCAGCTGTTCACCTGGACCCGCTT 2393
Qy 734 eProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheValPheAsnLeuAr 754
Db 2394 CCCGCTGTGGTACCGCCAGGCCCTCAGAGCATCTCTGCTGGCAGCTTCGTCCTCAACCTCCG 2453
Qy 754 gTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAlaSerThrAlaVa 774
Db 2454 CTGGGCAGAAAGCACAGAAAGTGGCGGTGAACCCATGGTGGTGACGGCAAGCACAGCTGT 2513
Qy 774 lAlaValThrValAspLysArgThrAlaIleAlaAlaAlaGlyValGlnMetLysLe 794
Db 2514 GCGCGTGACCGTGACAAAGGACAGCCATTTGTCAGCCCGCGCGGTCCAAATGAAGCT 2573
Qy 794 uGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThrValAspGlyPr 814
Db 2574 GGAATTCCTCCAGCGCAATTCGGCGGCAACCGGCGAGTGCAGACACTGTGGATGGGCC 2633
Qy 814 oTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAspAsnAenGlyPh 834
Db 2634 GTGCACACAGAGCTGCGAGGACAGTGATCTGGACTGCTTCGTATCGACAAACACAGCGGTT 2693
Qy 834 eIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGluValAspGlyAl 854
Db 2694 CATTCGTATCTCCAAGAGGTCCCGAGAGACGGGAAGATTTCTGGGGGAGGTGGATGTGC 2753
Qy 854 aValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMetTyrAspTyrGl 874
Db 2754 TGTCTCAGCCAGCTGCTCAGCATGGGGTGTTCAGCCAGTGACTATGTATGACTATCA 2813
Qy 874 nAlaMetCysLysProSerSerHisHisSerAlaAlaGlnProLeuValSerProIl 894
Db 2814 GGCCATGTGAAACCTCTAGTCAACCAACAGTGCAGCCAGCCCTGTGTGACGCCAAT 2873
Qy 894 eSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValLeuPheLeuLeuGl 914
Db 2874 TTTGCGCTTCTTGACGGCGACAGGTGGCTGCTGCAGAGCTGTGTCTCTCTCTGGGA 2933
Qy 914 uTrpSerValTrpGlySerTrpTyrAspArgGlyValAlaGluAlaLysSerValPheHisHi 934
Db 2934 GTGGAGTGTCTGGGGCTCTCTGTATGACAGACAGGGGGCGAGGCCAAAGTGTCTTCCATCA 2993
Qy 934 sSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGluTyrProValPh 954
Db 2994 CTCCCAAAACACAAAGAAGCAGGACCGCGCTGCAGCCCTGCGACAGGAGTACCCCGTGT 3053
Qy 954 eValTyrGlnProAlaIleArgGluAlaAenGlyIleValGluCysGlyProCysGlnLy 974
Db 3054 CGTGTACAGCGCGCCATCCGGGAGGCCAACGGGATCGTGAGTGGCGGCGCTCCAGAA 3113
Qy 974 sValPheValValGlnGlnProAenSerAsnLeuLeuLeuValThrAspProTh 994
Db 3114 GGTATTGTGGTGAGCAGATTCCTCAACAGTAACCTCTCTCTCTGTGTGACAGACCCAC 3173
Qy 994 rCysAspCysSerIlePheProValLeuGlnGluAlaThrGluValLysTyrAsnAl 1014
Db 3174 CTGTGACTGCAGCATCTTCCACCAGTGTGTGCAGGAGCGCAGAGTCAAAATAATGC 3233
Qy 1014 aSerValLysCysAspArgMetArgSerGlnLysLeuArgProAspSerCysHi 1034
Db 3234 CTCTGTCAAAATGTACCGGATGCCCTCCAGAACTCCGCGGCGACAGACTCTCTGCCA 3293

Qy 1034 sAlaPheHisProGluValArgValGluAlaAspArgGlyTrpAla 1049
Db 3294 CGCCTTCCATCCAGAGGAGAAATGCCAG---GACTGCGCGCGCGCC 3336

RESULT 7

AAS01432
ID AAS01432 standard; cDNA; 3209 BP.

XX AAS01432;

DT 04-JUL-2001 (first entry)

XX Human secreted soluble alpha2delta calcium channel subunit #17 cDNA.

Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;
alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;
gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;
filter binding assay; wheat germ lectin flashplate assay; ss.

XX Homo sapiens.

PH Key Location/Qualifiers

FT CDS 3..3209

FT /partial

FT /product= "Alpha2delta calcium channel subunit #17"

FT /note= "This sequence lacks a stop codon"

XX WO200119870-A2.

XX 22-MAR-2001.

XX 18-SEP-2000; 2000WO-EP009137.

XX 16-SEP-1999; 99US-00397550.

XX (WARN) WARNER LAMBERT CO.

XX Brown JP, Bertelli F;

XX WPI; 2001-235262/24.

XX P-PSDB; AAU01037.

Calcium channel alpha2delta subunits, useful in e.g. SPA assays.
Flashplate assays, Nickel Flashplate assays, Filter binding assays or
Wheat Germ Lectin Flashplate assays.

XX Claim 39; Page 147-148; 160pp; English.

The present sequence encodes for human secreted calcium channel
alpha2delta subunit #17 which is soluble and retains the functional
characteristics of the full length or wild type alpha2delta subunit
(AAU01025) from which it is derived. The invention relates to truncated
alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins
which retain their affinity for radioactively labelled gabapentin. The
alpha2delta subunit is 1 of the components of the heteromultimeric
voltage-dependent calcium channel (VDCC) complexes present in neuronal
and non-neuronal tissues including heart and skeletal muscle. Numerous
soluble forms of the human calcium channel alpha2delta subunits (AAU01014
-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the porcine
calcium channel alpha2delta subunits (AAU01027-AAU01031) are described.
The secreted soluble alpha2delta subunit may be used in assays e.g.
scintillation proximity assay (SPA), flashplate, nickel flashplate,
filter binding or wheat germ lectin flashplate assays to detect or
measure the binding or interaction of a ligand (e.g. gabapentin, L-
Norleucine, L-Allo-Isoleucine, L-methionine, L-Leucine, L-Isoleucine, L-
valine, Spermine and/or L-Phenylalanine) of a calcium channel alpha2delta
subunit

XX SQ Sequence 3209 BP; 757 A; 888 C; 920 G; 644 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	3209
Score:	5276.00	Matches:	1008
Percent Similarity:	99.70%	Conservative:	1
Best Local Similarity:	99.60%	Mismatches:	3
Query Match:	92.14%	Indels:	0
DB:	4	Gaps:	0
US-09-833-222A-10 (1-1090) x AAS01432 (1-3209)			
QY	11	AspArgValLysLeuTrpAlaAspThrPheGlyAspLeuTyrAsnThrValThrLys	30
DB	174	GAACACGTGAGCTATGGCTGACACCTTCGGGGGACCTGTATACACTGTGACCAA	233
QY	31	TyrSerGlySerLeuLeuGlnLysLysValGlyAspValGluSerSerLeuLysLe	50
DB	234	TACTCAGGCTCTCTCTGCTGCGAGAGATGACAGGATGAGGTCAGTCTGAGATC	293
QY	51	GluGluValAspGlyLeuGluValArgLysPheSerGluAspMetGluAsnMetLeu	70
DB	294	GAGGAGTGGATGGCTTGGAGCTGGTGAGGAGTTCTCAGAGGACATGGAGACATG	353
QY	71	ArgArgLysValGluAlaValGlnAsnLeuValGluAlaGluAlaAspLeuAsn	90
DB	354	CGGAGGAAAGTCGAGGCGGTCAGAACTCGTGGAGCTGCCGAGGAGCGCACCTGA	413
QY	91	HisGluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuLysLeuArg	110
DB	414	CACGAATTCATGATCCCTGGTGGTTCGACTATTACAACTCGGTCTGATCAACGAG	473
QY	111	AspGluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHis	130
DB	474	GACGAGAAGGCAACTTTCGTGGAGCTGGGCGCCGAGTTCTCTCGTGGATCCCATG	533
QY	131	PheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyr	150
DB	534	TTCAGCAACCTGCGGTGGAACCTCCATCAGCAGCGTGCAGCTGCCACCAACGTGTAC	593
QY	151	AsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPhe	170
DB	594	AACAAGACCCAGATATTTAAATGGAGTCTACATGCTGAAAGCTTGAATGCTGCTTC	653
QY	171	ValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGly	190
DB	654	GTGGAGAACTTCCAGAGAGACCCAAACGCTGACCTGGCAATATTTTGGCAGTGCAC	713
QY	191	PhePheArgIleTyrProGlyIleLysTrpThrPProAspGluAsnGlyValIleThrPhe	210
DB	714	TTCTTTCAGGATCTATCCAGGTATAAATGGACACCTGATGAGAATGGAGTCAATAC	773
QY	211	AspCysArgAsnArgGlyTyrTyrIleGlnAlaAlaThrSerProLysAspIleValIle	230
DB	774	GACTGCCAAACCGCGCTGATCATATTCAAGCTGCTACTTCTCCCAAGGACATAGTAT	833
QY	231	LeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIle	250
DB	834	TTGGTGGACGTGAGCGGCAGTATGAGGGGCTGAGGATGACTATTGCCAAGCACCATC	893
QY	251	ThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAsp	270
DB	894	ACCACCATCTTGGACACCCCTGGGGGAGAATGACTTCGTTAATATCATAGCGTCAATG	953
QY	271	TyrValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsn	290
DB	954	TAGTCCATTCATCGAGCTTGTGTTTAAAGGATCTCTGTCAGGGCGGACCGAGACAT	1013
QY	291	ArgGluHisPheLysLeuValGluLeuMetValLysGlyValGlyValValAsp	310
DB	1014	CGAGAGCATTTCAAACTGCTGGTGGAGAGTTCGATGCTCAAAAGTGTGGGGCGTGGAC	1073
QY	311	GlnAlaLeuArgGluAlaPheGlnIleLysGlnPheGlnGluAlaLysGlnGlySer	330
DB	1074	CAAGCCCTGAGAGAGCTTCCAGATCTTGAAGCAGTTCCAAAGGCGCAAGCAAGGAAG	1133

QY	331	LeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProVal	350
DB	1134	CTCTGCAACACGAGCCATCATGCTCATCGGACGGCGCGTGGAGGACTACGAGCCGGTG	1193
QY	351	PheGluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrIleuIleGlyArg	370
DB	1194	TTTGAGAGATATAACTGGCCAGACTGTAAAGTCCGAGTTTCTACCTCAATGGGAGA	1253
QY	371	GluValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThr	390
DB	1254	GAAGTGTCTTTTGTCTGACCGCATGAATGGATGTCATGCAACCAAGAGGCTACTACAG	1313
QY	391	GlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrIleuHisValLeuSer	410
DB	1314	CAGATCTCAACGCTGGCGGACCCAGGAGAACGTGATGGAATACCTGCACGTCTCAGC	1373
QY	411	ArgProMetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSer	430
DB	1374	CGCCCCATGTCTCAACCAACGACACGACATCATCTGGACAGAGGCTTACATGGACAGC	1433
QY	431	LysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProVal	450
DB	1434	AGCTCTCAGCTCGCAGGCTCAGAGCTGACACTGCTACCACTGTGGCCATGCCAGTC	1493
QY	451	PheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp	470
DB	1494	TTCAGCAAGAAAGAACCGCATCCCATGGCATTTCTCTGGGTGTGGTGGCTCAGAT	1553
QY	471	ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrIleLysLeuGlyValHisGlyTyr	490
DB	1554	GTGGCCCTCAGAGAGCTGATGAAGCTGGCGCCCGGTACAAGCTTGGAGTGCACGATAC	1613
QY	491	AlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr	510
DB	1614	GCCTTTCTGAACACCAACCAATGGCTACATCTCTCCCATCCCCGACCTCCGCGCCCTGTAC	1673
QY	511	ArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluVal	530
DB	1674	AGNAGGGGAGAAACCTAAACCCAAACCTAACTACACAGCTGGATCTCTCCGAAGTG	1733
QY	531	GluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr	550
DB	1734	GAGTGGGAAACACGAGCTGAATCTCTGAGAACACCATGATCAATAGGGAACAGGTACT	1793
QY	551	LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn	570
DB	1794	CTCTCATGATGTGAAGGTTCGATGGATAAAGGAAGCGAGTTCTTTTCTCGACCAAT	1853
QY	571	AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg	590
DB	1854	GACTACTCTTTCACGACATCAGCGACACCCCTTTTTCAGTTTGGGGTGGTGTCTCCCGG	1913
QY	591	GlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeu	610
DB	1914	GGCCACGAGAAATACATCTCTTCTGGGGAACACGCTCTGTGGAAGAAGGCTGCAATG	1973
QY	611	LeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspPro	630
DB	1974	CTTACCCACAGACTGGCCCTGGCGGTGACTGGATCTATCTGCATCAGATATTTGACCCA	2033
QY	631	AspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspPro	650
DB	2034	GACCACCGGAAGCTCAGCCAGCTAGAGGCCATGATCCGCTTCTCTACCGAAGGACCCA	2093
QY	651	AspLeuGluCysAspGluLeuValArgGluValLeuPheAspAlaValThrAla	670
DB	2094	GACCTGGAGTGTACGAGGAGCTGGTCCGGAGGTCTGTTCACCGGTGGTGACAGCC	2153
QY	671	ProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisVal	690
DB	2154	CCCATGGAGCCCTACTGGACAGCGCTGGCCCTCAACATGTCGAGGAGGTCTGAAACAGTG	2213
QY	691	ValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGly	710


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Db 2214 GTGACATGGCCCTTCCTGGGACCCGGGCTGGCCCTCCTGAGAAGCAGCTTGTTCGTGGGC 2273
Qy SerGluIysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThr 730
Db 2274 TCCGAGAAAGTCTCCGACGAGAAGTCTTGACACTGAGGACGAGGCGAGCGTGTTCACC 2333
Qy LeuAspArgPheProLeuTyrArgGlnAlaSerGluHisProAlaGlySerPheVal 750
Db 2334 CTGGACCGCTTCCCGCTGTGGTACCGCCAGGCTCAGAGCATCTGCTGGCAGCTTCGTC 2393
Qy PheAsnLeuArgTyrAlaGluGlyProGluSerAlaGlyGluProMetValValThrAla 770
Db 2394 TTCAACCTCCGCTGGGCGAGAGGACCAAGAAAGTCCGGGTGAACCATGGTGGTACCGGCA 2453
Qy SerThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAlaAlaGlyVal 790
Db 2454 AGCACAGCTGGCGGTGGTACCGTGGACAGAGGACAGCCATTGCTGCAGCGCGGGGCTC 2513
Qy GlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThr 810
Db 2514 CAAATGAAGCTGGAATTCCTCAGCGCAAAATTCCTGGCGGCAACGCGCAGTCAGCACT 2573
Qy ValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAsp 830
Db 2574 GTGGATGGCGCGTGCACACAGAGCTGCAGGACAGTGCATCTGGACTCTTCGTCTCATCGAC 2633
Qy AsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGlu 850
Db 2634 AACAAACGGTTCATCTGATCTCCAGAGGTCCCGAGAGCGGGAAGATTTCTGGGGAG 2693
Qy ValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMet 870
Db 2694 GTGGATGGTGTGCTCTGACCCAGCTGCTCAGCATGGGGTGTTCAGCCAAAGTCACTATG 2753
Qy TyrAspTyrGlnAlaMetCysLysProSerSerHisHisSerAlaAlaGlnProLeu 890
Db 2754 TATGACTATCAGGCGCATGTGCAAAACCTTCGAGTCAACACACAGTGCAGCGCCAGCCCTG 2813
Qy ValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluValLeu 910
Db 2814 GTACAGCCCAATTCCTGCTTCGACCGGACCAAGTGGTCTGTCAGGAGCTGGTCTG 2873
Qy PheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSer 930
Db 2874 TTCCTGTGGAGTGGAGTGTCTGGGCTCCTGTGTACGACAGAGGGGCGGAGCCAAAGT 2933
Qy ValPheHisSerHisLysHisLysGlnAspProLeuGlnProCysAspThrGlu 950
Db 2934 GTCTTTCATCACTCCCAACAAACAAAGAGCAGGACCCGCTGCAGCCCTCGCACCGGAG 2993
Qy TyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGly 970
Db 2994 TACCCCTGTGTGTGTACCAAGCGGCCCATCCGGAGAGCCCAACGGGATCTGGAGTGGGG 3053
Qy ProCysGlnLysValPheValValGlnIleProAsnSerAsnLeuLeuLeuVal 990
Db 3054 CCCTGCCAGAGGATTTGTGGTGCAGCAGATTCCTCCCAACAGTAACCTCTCTCTCTG 3113
Qy ThrAspProThrCysAspCysSerIlePheProValLeuGlnGluAlaThrGluVal 1010
Db 3114 ACAGACCCCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3173
Qy LysTyrAsnAlaSerValLysCysAspArgMetArg 1022
Db 3174 AATATATAGTCCCTCTGTCAAAATGTGACCGGATGGGC 3209
RESULT 8
AAF57569
ID AAF57569 standard; DNA; 3209 BP.
XX
AC AAF57569;
XX
```

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DT 11-JUN-2001 (first entry)
XX Human calcium channel alpha2delta subunit encoding DNA.
DE
XX Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;
KW nervous system disorder; pain; epilepsy; anxiety; human; ds.
KW
XX Homo sapiens.
XX OS
XX Key Location/Qualifiers
XX CDS 3..3209
XX /*tag= a
XX WO200120336-A2.
XX
XX 22-MAR-2001.
XX
XX 18-SEP-2000; 2000WO-EP009136.
XX
XX 16-SEP-1999; 99US-00397549.
XX (WARN ) WARNER LAMBERT CO.
XX
XX Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;
XX WPI; 2001-257902/26.
XX P-PSDB; AAB62261.
XX
XX Competitive binding assay for screening ligands which bind a cerebral
XX cortical voltage-dependent calcium channel alpha2-delta-1 subunit, where
XX the ligands identified are useful for treating disorders of the nervous
XX system, including pain.
XX
XX Disclosure; Page 145-146; 158pp; English.
XX
XX The invention relates to a new method for screening ligands which bind a
XX cerebral cortical voltage-dependent calcium channel alpha2delta subunit,
XX preferably alpha2delta-1 subunit. The method comprises contacting a
XX secreted soluble recombinant alpha2delta-1 subunit with a ligand of
XX interest and a labelled compound which binds the subunit, followed by
XX measuring the level of binding of the labelled compound to alpha2delta-1
XX subunit. The method is useful for screening ligands, preferably
XX biologically active products that modulate a nervous system function,
XX which bind a cerebral cortical voltage-dependent calcium channel
XX alpha2delta-1 subunit. The ligands identified by the method are useful
XX for treating disorders of the nervous system, including pain, epilepsy
XX and anxiety. The present sequence represents a human calcium channel
XX alpha2delta subunit encoding DNA
XX
XX Sequence 3209 BP; 757 A; 888 C; 920 G; 644 T; 0 U; 0 Other;
```

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Alignment Scores:
Pred. No.: 0 Length: 3209
Score: 5276.00 Matches: 1008
Percent Similarity: 99.70% Conservative: 1
Best Local Similarity: 99.60% Mismatches: 3
Query Match: 92.14% Indels: 0
DB: 5 Gaps: 0
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US-09-833-222A-10 (1-1090) x AAF57569 (1-3209)

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Qy 11 AspArgValLysLeuTrpAlaAspThrPheGlyAspLeuTyrAsnThrValThrLys 30
Db 174 GAAACAGTGAAGCTATGGCTGACACCTTCGCGGGGACCTGTATACACTGTGACCAA 233
Qy 31 TyrSerGlySerLeuLeuGlnLysLysPheValGluSerSerLeuLysIle 50
Db 234 TACTCAGGCTCTCTCTTGTCTGCAGAGAAAGTACAAGATGTGGAGTCCAGTCTGAAGATC 293
Qy 51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu 70
Db 294 GAGGAGGTGGATGGCTTGGAGCTGTGGAGGAAGTTCTCAGAGGACATGGAGACATGCTG 353
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Qy	71	Arg	Gly	Ser	Val	Glu	Ala	Val	Ile	Asn	Leu	Val	Glu	Ala	Ala	Glu	Ala	Asp	Leu	Asn	90														
Db	354	CGG	AGG	AA	AGT	CG	AGG	CGG	TC	CAG	AA	TC	TGG	AA	GCT	CG	CAG	AGG	AGG	CG	CTCAAC	413													
Qy	91	His	Glu	Phe	Asn	Glu	Ser	Leu	Val	Phe	Asp	Tyr	Tyr	Asn	Ser	Val	Leu	Ile	Asn	Glu	Arg	110													
Db	414	CAC	GAA	TTT	CA	TGA	AT	CC	TGG	TGT	TG	ACT	TAT	TAC	AA	CT	CGG	TCC	TG	AT	CAACGAGG	473													
Qy	111	Asp	Glu	Leu	Val	Glu	Ala	Glu	Phe	Leu	Leu	Glu	Ser	Asn	Ala	His						130													
Db	474	GAC	GAG	AA	GGC	CA	AT	TC	TGG	AG	TGG	CG	CC	GAG	TT	TC	TC	TGG	AG	TCC	AA	TGCTTCAC	533												
Qy	131	Phe	Ser	Asn	Leu	Pro	Val	Asn	Thr	Ser	Ile	Ser	Ser	Val	Gln	Leu	Pro	Thr	Asn	Val	Tyr	150													
Db	534	TT	CAG	CA	AC	CT	GC	CG	TGA	AC	CA	CT	CAT	CAG	CAG	CG	TGC	AG	TGC	CC	CA	CGTGTAC	593												
Qy	151	Asn	Leu	Asp	Pro	Asp	Ile	Leu	Asn	Gly	Val	Tyr	Met	Ser	Glu	Ala	Leu	Asn	Ala	Val	Phe	170													
Db	594	AAC	AAA	GAC	CC	CAG	AT	AT	TT	AAA	TGG	AG	CT	TAC	AT	GT	TGA	AG	CG	TT	GAA	TGCTTCTC	653												
Qy	171	Val	Glu	Asn	Phe	Gln	Arg	Asp	Pro	Thr	Leu	Thr	Trp	Gln	Tyr	Phe	Gly	Ser	Ala	Thr	Gly	190													
Db	654	GTG	GAG	AA	CT	TC	CAG	AG	AC	CC	AA	CG	TGT	GA	CT	TGG	CA	TAT	TTT	TGG	CAG	TGCAACTTGG	713												
Qy	191	Phe	Phe	Arg	Ile	Tyr	Pro	Gly	Ile	Leu	Ser	Trp	Thr	Pro	Asp	Glu	Asn	Gly	Val	Ile	Thr	Phe	210												
Db	714	TT	CT	T	CAG	AT	CT	AT	CC	CAG	GT	AT	AAA	AT	TGG	AC	CT	GAT	GAG	AT	GAG	TCA	TACTTTT	773											
Qy	211	Asp	Cys	Arg	Asn	Arg	Ser	Gly	Trp	Tyr	Ile	Gln	Ala	Ala	Thr	Ser	Pro	Leu	Ser	Asp	Ile	Val	Ile	230											
Db	774	GAC	TGC	CG	AA	CC	CGG	CTG	TAC	AT	CA	AG	CT	G	CT	TT	CT	CC	CA	AGG	AC	AT	AGT	833											
Qy	231	Leu	Val	Asp	Val	Ser	Gly	Ser	Met	Leu	Gly	Leu	Arg	Met	Thr	Ile	Ala	Leu	His	Thr	Ile	250													
Db	834	TTG	TG	AG	CG	TG	AG	CG	GAT	AT	GA	AG	GG	CT	TG	AG	GAT	GA	CT	AT	T	TGCCAAGCAC	893												
Qy	251	Thr	Thr	Ile	Leu	Asp	Thr	Leu	Gly	Glu	Asn	Asp	Phe	Val	Asn	Ile	Ile	Ala	Tyr	Asn	Asp	270													
Db	894	ACC	ACC	AT	CT	TGG	AC	AC	CC	CT	GGG	GAG	AA	TG	ACT	TC	T	TA	TAT	CAT	GAT	CAATGAC	953												
Qy	271	Tyr	Val	His	Ser	Tyr	Ile	Glu	Pro	Cys	Phe	Leu	Ser	Gly	Ile	Leu	Val	Gln	Ala	Asp	Arg	Asn	290												
Db	954	TAC	GT	CCA	AT	TAC	AT	CG	AG	CC	TT	GT	TT	AAA	AG	GG	AT	CC	TC	GT	CC	AGG	CGG	CCGAGACAAT	1013										
Qy	291	Arg	Glu	His	Ser	Phe	Leu	Ser	Val	Glu	Leu	Met	Val	Leu	Ser	Gly	Val	Gly	Val	Val	Asp	310													
Db	1014	CG	AG	G	CA	TTT	CA	AA	CT	CT	CT	GT	GG	AG	GT	TG	AT	GT	TCA	AA	GT	TGGGGGT	CGTGGAC	1073											
Qy	311	Gln	Ala	Leu	Arg	Glu	Ala	Phe	Gln	Ile	Leu	Ser	Gln	Phe	Gln	Glu	Ala	Leu	Ser	Gln	Gly	Ser	330												
Db	1074	CA	AG	CC	CT	TG	AG	AA	GC	CT	TC	CAG	AT	CT	TGA	AG	CAG	TT	CC	AA	GAG	CC	CAAGCAAGGAAGC	1133											
Qy	331	Leu	Cys	Asn	Gln	Ala	Ile	Met	Leu	Ile	Ser	Asp	Gly	Ala	Val	Glu	Asp	Tyr	Glu	Pro	Val	350													
Db	1134	CT	CT	G	CA	AC	CAG	GC	CA	TAT	CT	CAT	CAG	CAC	GC	CG	CT	TGG	AG	GACT	AC	GAGCCGGT	1193												
Qy	351	Phe	Glu	Leu	Ser	Tyr	Asn	Trp	Pro	Asp	Cys	Leu	Val	Arg	Val	Phe	Thr	Tyr	Leu	Ile	Gly	Arg	370												
Db	1194	TTT	GAG	AA	G	T	A	A	CT	GC	C	A	G	T	G	T	A	A	GT	TCC	ACT	TAC	TGGGAGA	1253											
Qy	371	Glu	Val	Ser	Phe	Ala	Asp	Arg	Met	Lys	Trp	Ile	Ala	Cys	Asn	Asn	Leu	Ser	Gly	Tyr	Tyr	Thr	390												
Db	1254	GA	AG	T	GT	CT	TT	TG	T	G	CC	G	AT	TG	AG	T	GC	AT	G	CA	CA	CA	AA	GA	GG	CT	ACT	TAC	AC	G	1313				
Qy	391	Gln	Ile	Ser	Thr	Leu	Ala	Asp	Thr	Gln	Glu	Asn	Val	Met	Glu	Tyr	Leu	His	Val	Leu	Ser	410													
Db	1314	CAG	AT	CT	CA	AC	CG	T	GG	CG	GA	CAC	CC	CAG	GAG	AA	CG	TG	AT	TG	GA	AT	TAC	T	GC	AG	CT	G	CT	C	CAG	1373			
Qy	411	Arg	Pro	Met	Val	Ile	Asn	His	Asp	His	Asp	Ile	Leu	Trp	Thr	Glu	Ala	Tyr	Met	Asp	Ser	430													
Db	1374	CG	CCCC	AT	GG	T	CA	T	CA	AC	CC	AG	CA	CA	TAT	CT	TG	GA	CAG	AGG	CC	TAC	AT	TG	G	A	G	CC	T	CA	TG	G	A	CAGC	1433
Qy	431	Lys	Leu	Leu	Ser	Ser	Gln	Ala	Gln	Ser	Leu	Thr	Leu	Thr	Thr	Val	Ala	Met	Pro	Val	450														

Db	1434	AAAGCTCTCAGCTCGCAGGGCTCAGAGCCTGACACTCTCTCACCACCTGTGGCCATGCCAGTC	1493
Qy	451	PheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp	470
Db	1494	TTCAGCAAGAAAGAACGAACCGCATCCCATGGCATTTCTTGGTGTGTGGGCTCAGAT	1553
Qy	471	ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyr	490
Db	1554	GTGGCCCTGAGAGAGCTGATGAAGCTGGCGCCCGTCAAGCTTGAGTGCACGGATAC	1613
Qy	491	AlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr	510
Db	1614	GCCTTTCTGAACACCAACCAATGGCTACATCTCTCCCATCCCGACCTCGCGCCCTGTAC	1673
Qy	511	ArgGluClyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluVal	530
Db	1674	AGAGAGGGGAAGAAACTTAAACCCCAAACCTTAACCTAACAGTGTGATCTCTCCGAAGTG	1733
Qy	531	GluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr	550
Db	1734	GAGTGGGAAGACCAGGCTGAATCTCTGAGACACAGCCATGATCAATAGGGAACAGGTACT	1793
Qy	551	LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn	570
Db	1794	CTCTCGATGATGTGAAGGTTCGATGGATAAAGGAAGCGAGTCTCTTTCTCTGACCAAT	1853
Qy	571	AspTyrPhePheThrAspLeuSerAspThrProPheSerLeuGlyAlaValLeuSerArg	590
Db	1854	GACTACTCTTCACGAGACATCAGCAGACCCCTTCAGTTTGGGGTGTGTCTCCCGG	1913
Qy	591	GlyHisGlyLysTyrIleLeuLeuGlyValAsnThrSerValGluGluGlyLeuHisAspLeu	610
Db	1914	GGCCACGGAGATACATCTCTTGGGGGAACACGTCTGTGGAGAGAGCCCTGCATGACTTG	1973
Qy	611	LeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspLeuAspPro	630
Db	1974	CTTCACCCAGACCTGGCCCTGGCGGTGACTGGATCTACTGCATCAGATATTGACCCA	2033
Qy	631	AspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspPro	650
Db	2034	GACCACCGGAAGCTCAGCAGCTAGAGGGCATGATCCGCTTCTCTACCAAGGAAGACCCA	2093
Qy	651	AspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAlaValValThrAla	670
Db	2094	GACCTGGAGTGTACCGAGGAGCTGGTCCGGAGGTCTGTGTTCACCGGTGTGTGACAGCC	2153
Qy	671	ProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisVal	690
Db	2154	CCCATGGAGCCCTACTGGACAGCGCTGGCCCTCAACATGTCCGAGGAGTCTGAACACGTG	2213
Qy	691	ValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGly	710
Db	2214	GTGGACATGGCCCTTCCTGGGCACCCGGGGTGGCCCTCTGAGAAGCAGCTGTGTGTGGGG	2273
Qy	711	SerGluLysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThr	730
Db	2274	TCCGAGAAGGTCTCCGACAGGAAGTTCTCTGACACCTGAGGACGAGGCCAGCGTGTTCACC	2333
Qy	731	LeuAspArgPheProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheVal	750
Db	2334	CTGGACCGCTTCCCGCTGTGGTATCCGCCAGGCCCTCAGAGCATCTCTCTGGCAGTCTCGTC	2393
Qy	751	PheAsnLeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAla	770
Db	2394	TTCAACCTCCGCTGGGCAGAAAGACAGAAAGTGGCGGGTGAACCCATGTGTGTGACGGCA	2453
Qy	771	SerThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAlaAlaGlyVal	790
Db	2454	AGCACAGCTGTGGCGGTGACCTGTGGACAGAGGACAGCCATGTGTCTGACGCCCGCGCGTC	2513
Qy	791	GlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThr	810

Db 2514 CAATGAAGCTGGAAATTCCTCAGCGCAAAATTCCTGGCGGCAACCGCGCAGTGCAGCACT 2573
Qy ValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAsp 830
Db GTGGATGGCCGTGCACACAGAGCTGCAGGACAGTGTGCTGGACTGCTTCTGTCATCGAC 2633
Qy AsnAsnGlyPheIleLeuIleSerIysArgSerArgGluThrGlyArgPheLeuGlyGlu 850
Db AACACCGGGTTCATTCTGATCTCCAAAGAGTCCCGAGAGACGGGAAGATTCTCGGGGAG 2693
Qy ValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMet 870
Db GTGGATGGTGTCTGCTCCTACCCAGCTGCTCAGCATGGGGGTGTTTCAGGCAAGTACTATG 2753
Qy TyrAspTyrGlnAlaMetCysLysProSerHisHisSerHisAlaGlnProLeu 890
Db TATGACTATCAGGCCATGTGCAAAACCTCGAGTCACCAACACAGTCGAGCCAGCCCTG 2813
Qy ValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnLeuValLeu 910
Db GTACGCCCAATTCCTGCTTGTGACGGCGACCAAGTGGCTGCTGCAGGAGCTGGTGTG 2873
Qy PheLeuLeuGluTyrSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSer 930
Db TTCTGCTGGAGTGGAGTGTCTGGGGCTCTCTGGTACGACAGAGGGCCGAGCCCAAAAGT 2933
Qy ValPheHisHisSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGlu 950
Db GTCTTCATCACTCCCAAAACACAAAGACAGGACCCGCTGCAGCCCTGCGACAGGAG 2993
Qy TyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGly 970
Db TACCCCGTGTTCGTGTACAGCCGCGCATCCGGGAGGCGCAACGGGATGCTGGAGTGGCGG 3053
Qy ProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLeuLeuVal 990
Db CCCTGCCAAGAGGTATTTGTGGTGAGCAGATTCCTCAACAGTAACCTCTCTCTGTGTG 3113
Qy ThrAspProThrCysAspCysSerIlePheProValLeuGlnGluAlaThrGluVal 1010
Db ACAGACCCACCTGTGACTGCAGCATCTTCCACCAAGTGTGCTGCAGGAGCGCACAGAGTC 3173
Qy LysTyrAsnAlaSerValLysCysAspArgMetArg 1022
Db AAATATATGCTCTGTCAAAATGTGACCGGATGCGC 3209

RESULT 9
AAS17581
ID AAS17581 standard; cDNA; 3228 BP.
XX AAS17581;
AC AAS17581;
XX AAS17581;
XX AAS17581;
DT 26-FEB-2002 (first entry)
XX DNA encoding novel secreted protein #10.
DE Secreted protein; cytostatic; immunosuppressive; vulnery; vaccine;
XX anti-inflammatory; neuroprotective; nephrotropic; cardiovascular; human;
KW cancer; autoimmune disease; wound healing disorder; infection;
KW haematopoietic disorder; inflammatory disorder; infertility;
KW neurological disease; psychiatric disease; cardiovascular disease;
KW respiratory disease; renal; gastrointestinal; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
FH 1..3228
FT CDS
FT /*tag= a
FT /product= "Human secreted protein"
XX WO200179454-A1.
PN
XX
XX
XX

XX 11-APR-2001; 2001WO-US011797.
PF
XX
PR 13-APR-2000; 2000US-0196603P.
PR 24-APR-2000; 2000US-0199417P.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;
XX
XX WPI: 2002-061975/08.
DR P-PSDB; RAU09869.
XX

PT New secreted proteins or polypeptides, useful for treating e.g. cancer,
PT autoimmune diseases, wound healing disorder, infections, hematopoietic
PT disorders, inflammatory disorders, infertility, cancer.
XX

PS Claim 2; Page 41-42; 92pp; English.

XX The invention relates to an isolated novel secreted polypeptide (I) and
CC polynucleotide (II). (I) and (II) are useful for treating cancer,
CC autoimmune diseases, wound healing disorder, infections, haematopoietic
CC disorders, inflammatory disorders, infertility, neurological and
CC psychiatric diseases, cardiovascular diseases, respiratory diseases,
CC renal diseases, or gastrointestinal diseases. These may also be used to
CC treat diseases, abnormalities and disorders caused by abnormal
CC expression, production, function and/or metabolism of the genes, as
CC vaccines for inducing immunological response in a mammal, and in
CC screening methods for detecting the effect of added compounds on the
CC production of mRNA and polypeptide in cells. The polypeptides can be used
CC as immunogens to produce antibodies immunospecific for the polypeptides,
CC and to identify membrane-bound or soluble receptors. The polynucleotides
CC may be used as diagnostic reagents, in chromosome localisation studies,
CC and in tissue expression studies. The present sequence represents the
CC coding sequence of novel human secreted protein #10
XX

SQ Sequence 3228 BP; 749 A; 897 C; 932 G; 650 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 3228
Score: 5234.50 Matches: 1013
Percent Similarity: 95.68% Conservative: 7
Best Local Similarity: 95.03% Mismatches: 34
Query Match: 91.42% Indels: 13
DB: Gaps: 3

US-09-833-222A-10 (1-1090) x AAS17581 (1-3228)

Qy 12 ArgValLysLeuTrpAlaAspThrPheGlyAspLeuTyrAsnThrValThrLysTyr 31
Db 58 AGAGTGAAGCTATGGGCTGACACCTTCGGCGGGGACCTGTATAACACTGTGACCAATAC 117
Qy 32 SerGlySerLeuLeuGlnLysLysValGlyAspValGluSerSerLeuLysLeuGlu 51
Db 118 TCAGGCTCTCTCTGCTGCAGAGAAGTACAAGGATGTGGAGTCCAGTCTCAAGATCAG 177
Qy 52 GluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArg 71
Db 178 GAGTGTGATGGCTGGAGCTGGTGGAGGAGTCTCAGAGGACATGGAGAAATCTGCGG 237
Qy 72 ArgLysValGluAlaValGlnAsnLeuValGluAlaGluAlaAspLeuAsnHis 91
Db 238 AGGAAAGTCGAGGCGGTCCAGAATCTGGTGAAGCTGCCGAGGAGGCGGACCTGAACCC 297
Qy 92 GluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArgAsp 111
Db 298 GAATTCATGAATCCCTGGGTTCGACTATTACAACTCGGTCTGTATCAACGAGGAGGAC 357
Qy 112 GluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHisPhe 131
Db 358 GAGNAGGGCAACTTCGTGGAGCTGGGCGCCGAGTTCCTCTCTGGAGTCCATGTCTCACTTC 417

Qy 132 SerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyrAsn 151
Db AGCAACCTGCGGTGAACACCTCCATCAGCAGCGTGCAGCTGCCACCAACGTGTACAAC 477
Qy 152 LysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPheVal 171
Db AAGACCCAGATATTTAAATGGAGTCTACATGTCTGAAGCCTTGAATGTCTTCGTG 537
Qy 172 GluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhe 191
Db GAGAACTTCCAGAGAGACCCAACTGTGACCTGGCAATATTTTGGCAGTGCACCTGGAACTC 597
Qy 192 PheArgIleTyrProGlyIleLeuTyrTrpThrProAspGluAsnGlyValIleThrPheAsp 211
Db TTCAGGATCTATCCAGGTATAAAATGGACACCTCATGAGAATGGAGTCATTTTGTGAC 657
Qy 212 CysArgAsnArgGlyTyrTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIleLeu 231
Db TGCCGAAACCGCGCTGGTACATTCAAAGCTGCTACTTCTCCCAAGGACATAGTGAAATTTG 717
Qy 232 ValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThr 251
Db GTGAGCTGTGCGCGAGTATGAAGGGCTGAGGATGACTATTGCCAAGGACACCATCAC 777
Qy 252 ThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAspTyr 271
Db ACCATCTTGGACACCTTGGGGAGAAATGACTTTCATTAATATCATAGCTACATGACTAC 837
Qy 272 ValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsnArg 291
Db GTCCATTTACATCGAGCCTTGTTTTAAAGGGATCCTCGTCAGGCGGACCGAGACAATCGA 897
Qy 292 GluHisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAspGln 311
Db GAGCATTTCAAACCTGCTGTGTGAGGAGTTGATGTCAAAGTGTGGGGTGTGTGGACCAA 957
Qy 312 AlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySerLeu 331
Db GCCCTGAGAGAAGCCTTCCAGATCCTCAAGCAGTTCCTCAAGAGGCCAAGCAAGGAAGCCTC 1017
Qy 332 CysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProValPhe 351
Db TGCAACCAAGCCATCATGCTCATCAGCGACGCGCGCTGTGAGGACTACGAGCGCGGTGTTT 1077
Qy 352 GluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrIleuIleGlyArgGlu 371
Db GAGAAGTATTAAGTGGCCAGACTGTAAAGTCCGAGTTCCTTACCTCATTTGGAGAGAA 1137
Qy 372 ValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThrGln 391
Db GTGTCTTTTGTGACCGCATGAAGTGGATTGATGATGCAATGCAACAAAGAGCTACTACGCGAG 1197
Qy 392 IleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrIleuHisValLeuSerArg 411
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RESULT 11
AAA09278
ID AAA09278 standard; cDNA; 5713 BP.
AC AAA09278;
XX
XX 10-AUG-2000 (first entry)
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XX Human alpha-2-delta-D gene splice variant 2.
XX
XX alpha-2-delta-D; calcium channel; 12p13.3; gabapentin; cytostatic;
XX KW anticonvulsant; antimigrane; antiparkinsonian; antidepressant;
XX KW splice variant; ss.
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XX Homo sapiens.
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XX 13-APR-2000.
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XX PF
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PR 30-OCT-1998; 98US-0106473P.
PR 29-DEC-1998; 98US-0114088P.
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XX (WARN ) WARNER LAMBERT CO.
XX
XX Johns MA, Moldover B, Offord JD;
XX PI
XX P-PSDB; AAY92323.
DR WPI; 2000-303744/26.
DR
XX
XX New human nucleic acids encoding the alpha2delta-C and alpha2delta-D
XX proteins, useful in the treatment of epilepsy, migraine, chronic pain,
XX anxiety, multiple sclerosis or cancer.
XX
XX Claim 22; Page 71-72; 88pp; English.
XX
XX The alpha-2-delta-D gene encodes a calcium channel subunit polypeptide.
XX The gene has been mapped to chromosome 12p13.1. This gene and the related
XX alpha-2-delta-C and -B genes are useful for protecting mammalian cells
XX from abnormal calcium flux by introducing expression vectors containing
XX the respective gene into mammalian cells. The antisense genes are also
XX useful for treating or preventing epilepsy. The alpha-delta-2-A protein
XX is a high-affinity binding target of the anti-convulsant drug gabapentin.
XX Therefore, alpha-delta-2 proteins may also be targeted to treat seizure-
XX related syndromes, migraine, ataxia, vestibular defects, chronic pain,
XX sleep interference, anxiety, amyotrophic lateral sclerosis (ALS), multiple
XX sclerosis, mania, tremor, parkinsonism, substance abuse or addiction
XX syndromes, mood, depression or cancer.
XX
XX SQ Sequence 5713 BP; 1397 A; 1570 C; 1548 G; 1195 T; 0 U; 3 Other;

Alignment Scores:
Pred. No.: 0 Length: 5713
Score: 5197.50 Matches: 1032
Percent Similarity: 80.87% Conservative: 4
Best Local Similarity: 80.56% Mismatches: 30
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Qy	711	SerGluLysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThr	730
Db	2274	TCCGAGAAGGTCTCCGACAGGAAGTTCTTGACACCTGAGGACGAGCGCGTTCACC	2333
Qy	731	LeuAspArgPheProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheVal	750
Db	2334	CTGGACCGCTTCCCGTGTGTGTAACCCAGCGCTCAGAGCATCTCTGCTGCGAGCTTCGTC	2393
Qy	751	PheAsnLeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAla	770
Db	2394	TTCAACCTCCGCTGGCGAAGACCCAGAAAGTGGCGGGTGAACCCATGGTGGTGACGGCA	2453
Qy	771	SerThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAlaAlaGlyVal	790
Db	2454	AGCAGACGCTGTGGCGGTGACCGTGGACACAGAGGACAGCCATTTGCTGCACCGCGGGCGTC	2513
Qy	791	GlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThr	810
Db	2514	CAAAATGAAGCTGGAATTCCTCCAGCGCAAAATTCGGCGCGCAACGCGGCGAGTGCAGCACT	2573
Qy	811	ValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAsp	830
Db	2574	GTGGATGGGCCGTGCACAGAGCTCGAGGACAGTGATCTGGAGCTGCTTCGTGCATCGAC	2633
Qy	831	AsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGlu	850
Db	2634	NACNACGGGTTCATTCTGATCTCCAAGAGTCCCGAGAGCGGGAAGATTTTCTGGGGGAG	2693
Qy	851	ValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMet	870
Db	2694	GTGGATGGTGTGCTCTCGACCCAGCTGCTCAGCATGGGGGTGTTCAGCCAAAGTGACTATG	2753
Qy	871	TyrAspTyrGlnAlaMetCysLysProSerSerHisHisSerAlaAlaGlnProLeu	890
Db	2754	TATGACTATCAGGCCATGTGCANAAACCTTCAGTCCACACACAGTGCAGGCCAGCCCGCTG	2813

Qy	891	ValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnLeuValLeu	910
Db	2814	GTCAAGCCCAATTTCTGCTTCTTACCGCGACCAAGGTGGCTGCTGCAGGAGCTGGTCT-	2872
Qy	910	-----	910
Db	2873	TGTGAGTGGGGGTAGACACGGGGCTGGTGGAGGCTGCATGCGAGGGTGGCTTAGAGAGGT	2932
Qy	910	-----	910
Db	2933	GTCTTGTATCAGGAGGCTGCAAGGTCTCAGGACAAACCACTTGTCTACCAAGACCCCGG	2992
Qy	910	-----	910
Db	2993	GAAGGAGGCAACAATCCCTGGGCATGAGACGCCACTCTTCCCTGCATGCTTGGCCCTGG	3052
Qy	910	-----	910
Db	3053	AGGGACCTCATTTGCTCAACACAGAGCCCTCAAGCAGGAGAGGGTGTCTTGGAGGAGG	3112
Qy	910	-----	910
Db	3113	GGATGGCCGGGGCTGTTCAGGATACTCCAGCTCTTGGGAACCCAAAGTCGGGAGGCT	3172
Qy	911	-----PheLeuLeuGluTrpSerValTrp	918
Db	3173	CAGAGGTCCTCCGAGATTCACTCTGTGTGACAGAGTTCTCTGCTGGAGTGGAGTCTGG	3232
Qy	919	GlySerTrpTrpAspArgGlyValaglu-----	927
Db	3233	GGCTCTGGTACGACAGAGGGGCCGGGTGAGTCACGGAGCTGCAGGGCCATGTCTGT	3292
Qy	927	-----	927
Db	3293	AAGAGCAGTGGCAATTTTGGTCCACTAAGCTGAGACCACTTCCCTGTGGGTGGGTGACAGT	3352
Qy	927	-----	927
Db	3353	GGGGATAGGTGACCCCTGAAGCATCGTTTTCACATCTCACCTTGCCTTCTCTCAT	3412
Qy	927	-----	927
Db	3413	CACATCCCTCACTCCTGGCTGTGTGTGACATCATCTTGGGACACCGCCACTCCATGTG	3472
Qy	927	-----	927
Db	3473	CCATCATCACACCCCATGACATCTGCCCTCATGTGCCACCATGTTTTCTGTGCCGTG	3532
Qy	928	-----AlaLysSerValPheHisHisSerHisLys	937
Db	3533	TCCACCCTGTCTGGGCTTATGTTTCGGCCAGCCAAAGTGTCTTCCATCACTCCCAAA	3592
Qy	937	sHisLysLysGlnAspProLeuGlnProCysAspThrGluTyProValPheValTyGln	957
Db	3593	ACACAAAGACAGACCCGCTGTCAGCCCTGCGACACGGAGTACCCCGTGTTCGTGTACCA	3652
Qy	957	nPro-AlaIleArgGluAlaAsnGlyIleValGluCysGlyProCysGlnLysValPheV	977
Db	3653	CGCGGNCATCCCGGAGGCCAACGGGATCTGTGGAGTGGGGCCCTCGCACAGAGGTATTG	3712
Qy	977	alValGlnGlnIleProAsnSerAsnLeuLeuLeuValThrAspProThrCysAspC	997
Db	3713	TGGTGCAGCAGATTCCCAACAGTAACCTCTCTCTCTGGTGACAGACCCACCTGTGACT	3772
Qy	997	ysSerIlePheProProValLeuGlnGlnIleThrGluValLysTyAsnAlaSerValL	1017
Db	3773	GCAGCATCTTCCCAACAGTGTGCGAGAGCGCAGAAAGTCAAATATAATGCCTCTGTCA	3832
Qy	1017	ysCysAspArgMetArgSerGlnLysLeuLeuArgArgProAspSerCysHisAlaPheH	1037
Db	3833	AATGTACCGGATGCGCTCCAGAGCTCCGCGCGGACACAGACTCTGCGACGCGCTTCC	3892
Qy	1037	isProGluValArgValGluAlaAspArgGlyTrpAlaGlyPheSerSerProAsnProL	1057

[illegible]


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Qy 671 ProMetGluAlaTyrTrpThrAlaLeuAlaLeuMetSerGluGluSerGluHisVal 690
Db 2154 CCCATGGAAGCCTACTGGACAGCGCTGGCCCTCAACATGTCGAGGAGTCTGAACAGTG 2213
Qy 691 ValAspMetAlaPheLeuGlyThrArgAla----- 700
Db 2214 GTGGACATGGCCTTCTGGGACACCGGGCTGGCCCTCTGAGAAGCAGCTGTTCGTGGGC 2273
Qy 701-----GlyLeuLeuArgSerSerLeuPheValGlySerGluLysVa 714
Db 2274 TCCGAGAAGGTCTCCGAGTGGCCTCTCTGAGAAGCAGCTTGTTCGTGGCTCCGAGAAGGT 2333
Qy 714 iSerAspArgLysPheLeuThrProGluAaspGluAlaSerValPheThrLeuAspArgPh 734
Db 2334 CTCCGACAGAAGTTCCTGACACCTGAGGACGAGCGAGCGTGTTCACCTGGACCGCTT 2393
Qy 734 eProLeuTyrTrpArgGlnAlaSerGluHisPheAlaGlySerPheValPheLeuLeuAr 754
Db 2394 CCGCTGTGTACCGCCAGCGCTCAGAGCATCTCTGCTGGCAGCTTCTCTTCAACCTCCG 2453
Qy 754 gTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAlaSerThrAlaVa 774
Db 2454 CTGGCAGAGAAGGACCAAGAGTGGGGTGAACCCATGCTGGTGGTGGCAGCGCAAGCAGCTGT 2513
Qy 774 lAlaValThrValAspLysArgThrAlaAlaAlaAlaGlyValGlnMetLysLe 794
Db 2514 GCGGTGACCGTGGACAGAGGACAGCCATTTGCTGCAGCGCGCGGCGTCCAAATGAAGCT 2573
Qy 794 uGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThrValAspGlyPr 814
Db 2574 GGAATTCCTCAGCGCAAAATTCGGCGGCAACCGCGCAGTGTGACGACTGTGTGATGGGCC 2633
Qy 814 oTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAspAenAenGlyPh 834
Db 2634 GTGCACACAGAGCTGCGAGGACAGTGATCTGGACTGCTTCTCATCGACACACCGGTT 2693
Qy 834 eLleLeuLysSerLysArgSerArgGluThrGlyArgPheLeuGlyGluValAspGlyAl 854
Db 2694 CATTCGATCTCCAAAGAGTCCCGAGAGCGGGAAGATTTCGGGGAGGTGGATGGTGC 2753
Qy 854 aValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMetTyrAspTyrGl 874
Db 2754 TGTCTGACCGAGCTGCTCAGCATGGGGGTGTTCCGCCAAGTGACTATGATGACTATCA 2813
Qy 874 nAlaMetCysLysProSerSerHisHisSerAlaAlaGlnProLeuValSerProIl 894
Db 2814 GGCCATGTGCAAAACCTCGAGTCACACACAGTGCAGCCAGCCCTGCTGTCAGCCCAAT 2873
Qy 894 eSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluValLeuPheLeuGlu 914
Db 2874 TTCTGCCCTTCTTGACGGCGACAGGTGGCTGCTGCAGGAGCTGTGTCTCTGCTGGA 2933
Qy 914 uTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSerValPheHisHi 934
Db 2934 GTGAGTGTCTGGGGCTCTCTGGTACGACAGAGGGCGCGAGCCAAAGTGTCTTCCATCA 2993
Qy 934 sSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGluTyrProValPh 954
Db 2994 CTCCCAACACACAGAAGCAGGACCGCTGCGACCTGCGACACCGAGTACCCCGTGT 3053
Qy 954 eValTyrGlnProAlaIleArgGluAlaAenGlyIleValGluCysGlyProCysGlnLy 974
Db 3054 CGTGTACAGCCGCGCATCCGGAGGCGCAACGGGATCGTGGAGTGGCGGCGCTGCCAGAA 3113
Qy 974 eValPheValValGlnGlnIleProAenSerAenLeuLeuLeuValThrAspProTh 994
Db 3114 GGTATTTGTGGTGAGCAGATTTCCAAACAGTAACCTCTCTCTCTGTGTGACAGACCCAC 3173
Qy 994 rCysAspCysSerIlePheProProVal 1003
Db 3174 CTGTGACTGCGAGCATCTTCCACCAGTG 3201
```

RESULT 13

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AAF57568
ID AAF57568 standard; DNA; 3201 BP.
XX AC AAF57568;
XX DT 11-JUN-2001 (first entry)
XX DE Human calcium channel alpha2delta subunit encoding DNA.
XX KW Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;
XX KW nervous system disorder; pain; epilepsy; anxiety; human; ds.
XX OS Homo sapiens.
XX PN WO200120336-A2.
XX PD 22-MAR-2001.
XX PF 18-SEP-2000; 2000WO-EP009136.
XX PR 16-SEP-1999; 99US-00397549.
XX PA (WARN ) WARNER LAMBERT CO.
XX PI Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;
XX DR WPI; 2001-257902/26.
XX PT Competitive binding assay for screening ligands which bind a cerebral
XX PT cortical voltage-dependent calcium channel alpha2-delta-1 subunit, where
XX PT the ligands identified are useful for treating disorders of the nervous
XX PS system, including pain.
XX PS Disclosure; Page 144-145; 158pp; English.
XX CC The invention relates to a new method for screening ligands which bind a
XX CC cerebral cortical voltage-dependent calcium channel alpha2delta subunit,
XX CC preferably alpha2delta-1 subunit. The method comprises contacting a
XX CC secreted soluble recombinant alpha2delta-1 subunit with a ligand of
XX CC interest and a labelled compound which binds the subunit, followed by
XX CC measuring the level of binding of the labelled compound to alpha2delta-1
XX CC subunit. The method is useful for screening ligands, preferably
XX CC biologically active products that modulate a nervous system function,
XX CC which bind a cerebral cortical voltage-dependent calcium channel
XX CC alpha2delta-1 subunit. The ligands identified by the method are useful
XX CC for treating disorders of the nervous system, including pain, epilepsy
XX CC and anxiety. The present sequence represents a human calcium channel
XX CC alpha2delta subunit encoding DNA
SQ Sequence 3201 BP; 748 A; 888 C; 921 G; 644 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 3201
Score: 5148.00 Matches: 989
Percent Similarity: 98.02% Conservative: 1
Best Local Similarity: 97.92% Mismatches: 3
Query Match: 89.91% Indels: 17
DB: 5 Gaps: 1

US-09-833-222A-10 (1-1090) x AAF57568 (1-3201)
Qy 11 AspArgValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAenThrValThrLys 30
Db 174 GAAACAGTGAAGCTATGGCTGACACCTTCGGCGGGACCTGTGTATACACTGTGACCAA 233
Qy 31 TyrSerGlySerLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIle 50
Db 234 TACTCAGGCTCTCTTCTGTCTGCAGAAAGATGACAGGATGGAGTCCAGTCTGAAGATC 293
Qy 51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAenMetLeu 70
Db 294 GAGGAGTGGATGGCTTGGAGCTGTGAGGAAGTTCTCAGAGGACATGGAGACATGCTG 353
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Qy 71 ArgArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsn 90
Db 354 CGGAGGAAGCTCGAGGCGGTCAGAAATCGTGTGAAGCTGCCGAGGAGCGCACTGAAC 413
Qy 91 HisGluPheAsnGlnSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArg 110
Db 414 CACGAATTCGAATGAATCCCTGGTGTTCGACTATTACAACTCGGTCTTGATCAACGAGAGG 473
Qy 111 AspGluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHis 130
Db 474 GACGAGAAGGCAACTTCGTGGAGCTGGGCGCCGAGTTCTCTCGGAGTCCAATGCTCAC 533
Qy 131 PheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyr 150
Db 534 TTCAGCAACCTGCCGGTGAACACCTCCATCAGCAGCGTCGAGCTGCCACCAACGCTGAC 593
Qy 151 AsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPhe 170
Db 594 AACAAAGACCCAGATATTTTAAATGGAGTCTACATGTCTGAAGCCTTGAATGCTGTCTTC 653
Qy 171 ValGluAsnPheGlnArgAspProThrLeuThrTropGlnTyrPheGlySerAlaThrGly 190
Db 654 GTGGAGAACTTCCAGAGACCCCAACGTTGACCTGGCAATATTTTGGCAGTGAACCTGGA 713
Qy 191 PhePheArgIleTyrProGlyIleLysTyrThrProAspGluAsnGlyValIleThrPhe 210
Db 714 TTCTTCAGGATCTATCCAGGTATAAATGGACACCTGATGAGAAATGGAGTCAATACTTTT 773
Qy 211 AspCysArgAsnArgGlyTyrTyrIleGlnAlaAlaThrSerProLysAspIleValIle 230
Db 774 GACTCGCGAAACCGCGCTGTCATATTCAAGCTGCTACTTCTCCCAAGGACATAGTGATT 833
Qy 231 LeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIle 250
Db 834 TTGGTGAGCTGAGCGCGCAGTAGAAGGGGCTGAGGATGACTATGTCCAAAGCACACCATC 893
Qy 251 ThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAsp 270
Db 894 ACCACCATCTTGGACACCTTGGGGGAGAAATGACTTCGTGTAATATCATAGCGTACAAATGAC 953
Qy 271 TyrValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsn 290
Db 954 TAGCTCCATTACATTCGAGCCTTGTTTTAAAGGGATCCTCGTCAGCGCGGACCGAGACAAT 1013
Qy 291 ArgGluHisPheLysLeuLeuValGluLeuMetValLysGlyValGlyValValAsp 310
Db 1014 CGAGAGCATTTTCAAACCTGCTGGTGGAGGAGTTGATGTCAAAGGTGTGGGGGTCTGGGAC 1073
Qy 311 GlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySer 330
Db 1074 CAAGCCCTGAGAGAGCGCTTCCAGATCTTGAAAGCAGTTCCAAAGGCGCAAGCAAGAGAC 1133
Qy 331 LeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProVal 350
Db 1134 CTCTGCAACACGAGCCATCATGCTCATCAGCGCGCGCGCTGGAGGACTACGAGCCGGTG 1193
Qy 351 PheGluLysTyrAsnTyrProAspCysLysValArgValPheThrTyrLeuIleGlyArg 370
Db 1194 TTTGAGAAGATATAACTGGCCAGACTGTAAAGGTCCGAGGTTTTCCTTACCTCATTTGGGAGA 1253
Qy 371 GluValSerPheAlaAspArgMetLysTyrIleAlaCysAsnAsnLysGlyTyrTyrThr 390
Db 1254 GAAGTGTCTTTTGTGACCGCATGAAGTGAATGGATTCGATGCACCAACAAAGGCTACTACAG 1313
Qy 391 GlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSer 410
Db 1314 CAGATCTCAACGCTGGCGGACACCCAGGAGAACGCTGATGCAATACCTGCAACAAAGGCTACTACAG 1373
Qy 411 ArgProMetValIleAsnHisAspHisAspIleIleTyrThrGluAlaTyrMetAspSer 430
Db 1374 CGCCCCATGCTCATCAACACGACCCAGACATCATCTGGACAGAGGCTTACATGGACAGC 1433
Qy 431 LysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrValAlaMetProVal 450
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Db 1434 AAGCTCTCTCAGCTCGCAGGCTCAGAGCCTGACACTCTCACCACCTGTGGCCATGCCAGTC 1493
Qy 451 PheSerLysLysAsnGlnThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp 470
Db 1494 TTCAGCAAGAAGAACAAACGCGATCCCATGGCATTTCTCTGGGTGTGGTGGCTCAGAT 1553
Qy 471 ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyr 490
Db 1554 GTGGCCCTTGAGAGAGCTGATGAAGCTGGCGCCCCGGTACAAAGCTTGGAGTGCACGATAC 1613
Qy 491 AlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr 510
Db 1614 GCCTTTCTGAACACCAACAATGGCTACATCTCTCCCATCCCCGACCTCCGCGCCCTGTAC 1673
Qy 511 ArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluVal 530
Db 1674 AGAGAGGGGAAGAACTAAACCCCAACCTAACTACAACAGTGTGGATCTCTCCGAAGTG 1733
Qy 531 GluTyrGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr 550
Db 1734 GAGTGGGAAGACCAAGCTGAACTCTCTGAGAACAAGCCATGATCAATAGGGAACAAGGTACT 1793
Qy 551 LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn 570
Db 1794 CTCTCGATCGATGTGAAGGTTCCGATGGATAAAGGGAAGCGAGTTCTTTTCTTGACCAAT 1853
Qy 571 AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg 590
Db 1854 GACTACTTCTTACGGACATCAGCAGACACCCCTTTCAGTTTGGGGGTGGTGTCTCCCGG 1913
Qy 591 GlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeu 610
Db 1914 GGCCACGGAGAATACATCTTCTGGGGAACAAGCTCTGTGGAGAAGAGCCCTGCATGACTTG 1973
Qy 611 LeuHisProAspLeuAlaLeuAlaGlyAspTyrIleTyrCysIleThrAspIleAspPro 630
Db 1974 CTTTACCCAGACCTGGCCCTTGCGCGGTGACTGATCTACTGCATCACAGATATTGACCCA 2033
Qy 631 AspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspPro 650
Db 2034 GACCACCGGAAGCTCAGCAGCCTAGAGGCGCATGATCCGCTTCTCACAGGAAGGACCCA 2093
Qy 651 AspLeuGluCysAspGluLeuValArgGluValLeuPheAspAlaValValThrAla 670
Db 2094 GACCTGGAGTGTGACGAGGAGCTGTCTCCGGAGGCTCTGTTGACCGCGTGTGCACAGCC 2153
Qy 671 ProMetGluAlaTyrTyrThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisVal 690
Db 2154 CCCATGGAAAGCTTACTGGACAGCGCTGGCCCTCAACATGTCCGAGGAGTCTGAAACAGTG 2213
Qy 691 ValAspMetAlaPheLeuGlyThrArgAla----- 700
Db 2214 GTGGACATGGCTTCTCTGGGCACCCCGGCTGGCCTCTCTGAGAAGCAGCTGTTTCTGTGGGC 2273
Qy 701 -----GlyLeuLeuArgSerSerLeuPheValGlySerGluLysVal 714
Db 2274 TCCGAGAAGCTCTCCAGTGGCTCTCTGAGAAAGCAGCTTGTCTGTGGGTCTCCGAGAGGT 2333
Qy 714 lSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThrLeuAspArgPhe 734
Db 2334 CTCCGACAGGAAGTTCTCTGACACCTTGAGGACGAGGCGCAGCGTGTTCACCTCGACCGCTT 2393
Qy 734 eProLeuTyrTyrArgGlnAlaSerGluHisProAlaGlySerPheValPheAsnLeuAr 754
Db 2394 CCCGCTGTGGTACCAGGACCCAGGCGCTCAGAGCATCTCTGTGCAGCTTCTCTTCAACCTCCG 2453
Qy 754 gTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAlaSerThrAlaVal 774
Db 2454 CTGGGCGAAGAGACCAAGAAAGTCCGGGTGAACCCATGGTGTGGTGCACGCGCAAGCACAGCTGT 2513
Qy 774 lAlaValThrValAspLysArgThrAlaIleAlaAlaAlaGlyValGlnMetLysLe 794
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Db 2514 GCGGCTGACCGTGCACAGAGCAGCAGCATTTGCTGCAGCCCGCGCTCCAAATGAAGCT 2573

Qy 794 uGlupheLeuGlnArgLysPheThrAlaAlaThrArgGlnCysSerThrValAspGlyPr 814

Db 2574 GGAATTCCTCAGCGCAATTCCTGGCGGCAACCGCGCAGTGCAGCACTGTGGATGGGCC 2633

Qy 814 oTyThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAspAenAenGlyPh 834

Db 2634 GTGCACACAGAGCTGCAGGACAGTGTCTGGACTGTCTGCTATCGACACACACAGGGTT 2693

Qy 834 eIleLeuLeuSerLysArgSerArgGluThrGlyArgPheLeuGluValAspGlyVal 854

Db 2694 CATTCGTATCTCCAGAGGTCCTCCAGAGACGGGAAGATTTCTGGGGAGGTGGATGGTC 2753

Qy 854 aValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMetTyrAspTyrGI 874

Db 2754 TGTCTGACCCAGCTGCTCAGCATGGGGTGTTCAGCAAGTACTATGATGACTATCA 2813

Qy 874 nAlaMetCysLysProSerSerHisHisHisSerAlaAlaGlnProLeuValSerProII 894

Db 2814 GGCCATGTGCAAACTCGAGTCCACACACAGTGCAGCCCGCTGGTTCAGCCCAAT 2873

Qy 894 eSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValLeuPheLeuLeuGI 914

Db 2874 TTTGCTCTTTGACGGCAGCAGTGCTGCTCAGAGAGCTGTGTCTGCTGCTGGA 2933

Qy 914 uTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSerValPheHisH 934

Db 2934 GTGGAGTGTCTGGGGCTCTGGTACGACAGAGGGCGGCGGCAAAAGTGTCTTCCATCA 2993

Qy 934 sSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGluTyrProValPh 954

Db 2994 CTCCACAAACACAAAGAGCAGGACCGCTGTCAGCCCTGCGACACGGAGTACCCCGTGT 3053

Qy 954 eValTyrGlnProAlaIleArgGluAlaAenGlyIleValGluCysGlyProCysGlnLy 974

Db 3054 CGTGTACCGCGGCCATCCGGAGGCCAACGGGATCGTGAGTGGCGGCGCTCCAGAA 3113

Qy 974 sValPheValValGlnGlnIleProAenSerAsnLeuLeuLeuValThrAspProTh 994

Db 3114 GGATATTGTGGTGCAGCAGATTCCCAACAGTAACTCTCTCTCTGTGTGACAGACCCAC 3173

Qy 994 rCysAspCysSerIlePheProVal 1003

Db 3174 CTGTGACTGCAGCATCTCCACACAGTG 3201

RESULT 14

ID ADN33188 standard; DNA; 3742 BP.

AC ADN33188;

XX

XX 18-NOV-2004 (first entry)

XX Human transporter and ion channel (TRICH) gene SeqID73.

XX transporters and ion channel; TRICH; neuroprotective; relaxant;

KW antithyroid; antidiabetic; cytostatic; dermatological; immunosuppressive;

KW antiinflammatory; thymimetic; antiallergic; cerebroprotective;

KW gastrointestinal; hepatotropic; nephrotropic; anticonvulsant;

KW antiparkinsonian; antibacterial; antiparasitic; fungicide; protozoacide;

KW virucide; utropathic; antirheumatic; cardiant; cardiovascular; anti-HIV;

KW neotropic; TRICH agonist; TRICH antagonist; gene therapy;

KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;

KW muscular disorder; myotonic dystrophy; catatonia; endocrine disease;

KW diabetes; Grave's disease; cancer; leukaemia; cervical cancer;

KW breast cancer; immunological disorder; scleroderma;

KW systemic lupus erythematosus; allergy; gastrointestinal disorder;

KW Crohn's disease; renal disorder; Goodpasture's syndrome; infection;

KW viral; bacterial; fungal; parasitic; protozoal; helminthic;

KW cardiovascular disorder; atherosclerosis; hepatic disease; cirrhosis;

KW transgenic animal; gene; ds; human.

OS Homo sapiens.

XX WO2004035755-A2.

XX 29-APR-2004.

XX 16-OCT-2003; 2003WO-US033087.

PF 16-OCT-2002; 2002US-0419313P.

XX 23-OCT-2002; 2002US-0421033P.

PR 25-OCT-2002; 2002US-0421349P.

PR 04-NOV-2002; 2002US-0423516P.

XX (INCY-) INCYTE CORP.

XX Hafalia AJA, Khare R, Lal PG, Yue H, Baughn MR, Thornton MB;

PI Lu DAM, Ison CH, Becha SD, Ding L, Warren BA, Lee SY, Swarnakar A;

PI Elliott VS, Richardson TW, Marquis JP, Ramkumar J, Murage J;

PI Raumann BE, Yao MG, Lu Y, Gietzen KJ, Yang YG, Chang H, Chawla NK;

PI Tran UK, Lee S, Yang J, Gandhi AR, Tribouley CM, Policky JL;

PI Ring HZ, Lee EA;

XX WPI: 2004-348448/32.

DR P-PSDB; ADN33132.

XX New TRICH polypeptides, useful for diagnosing, preventing, and treating

PT disorders associated with abnormal expression or activity of TRICH, e.g.

PT neuromuscular, immunological, cardiovascular disorders, cancer and/or

PT infections.

XX Claim 5; SEQ ID NO 73; 285pp; English.

XX This invention relates to novel human transporters and ion channel

CC (TRICH) proteins and the nucleotide sequences which encode them. The

CC invention may be useful for the production of compounds with a

CC neuroprotective, relaxant, antithyroid, antidiabetic, cytostatic,

CC dermatological, immunosuppressive, antinflammatory, thymimetic,

CC antiallergic, cerebroprotective, gastrointestinal, hepatotropic,

CC nephrotropic, anticonvulsant, antiparkinsonian, antibacterial,

CC antiparasitic, fungicide, cardioacide, virucide, utropathic,

CC antirheumatic, cardiant, cardiovascular, anti-HIV or nootropic activity

CC acting as TRICH agonists or antagonists. In addition the disclosed

CC sequences may be useful for gene therapy. The invention may be useful in

CC diagnosing, preventing, and treating disorders associated with an

CC abnormal expression or activity of TRICH, such as neurodegenerative

CC disorders (for example Parkinson's disease, Alzheimer's disease),

CC muscular disorders (for example myotonic dystrophy, catatonia), endocrine

CC disorders (for example diabetes, Grave's disease), cancers (for example

CC leukaemia, cervical or breast cancers), immunological disorders (for

CC example scleroderma, systemic lupus erythematosus, allergies),

CC gastrointestinal disorders (for example Crohn's disease), renal disorders

CC (for example Goodpasture's syndrome), infections (for example viral,

CC bacterial, fungal, parasitic, protozoal, helminthic), cardiovascular

CC disorders (for example atherosclerosis), or hepatic diseases (for example

CC cirrhosis). TRICH or its fragments may also be used in screening for

CC compounds that specifically bind to and modulate the activity of TRICH.

CC The nucleotides can be used to create humanised animals or transgenic

CC animals to model human disease. The present sequence is that of a human

CC transporter and ion channel (TRICH) gene of the invention.

XX SQ Sequence 3742 BP; 882 A; 1052 C; 1053 G; 755 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 3742

Score: 5137.50 Matches: 998

Percent Similarity: 92.62% Conservative: 6

Best Local Similarity: 92.07% Mismatches: 31

Query Match: 89.55% Indels: 51

DB: 13 Gaps: 2

US-09-833-222A-10 (1-1090) x ADN33188 (1-3742)

Qy 11 AspArgValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAenThrValThrLys 30

Db 106 GAAACAGTGAAGCTATGGCTGACACCTTCGGCGGGACCTGTATACACTGTGACCAA 165
Qy 31 TyrsSerGlySerLeuLeuLeuGlnLysGlyTyrLysAspValGluSerSerLeuLysIle 50
Db 166 TACTCAGGCTCTCTCTGCTGCGAAGAAGTACAAGAGTGTGGAGTCCAGTCTGAAGATC 225
Qy 51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAenMetLeu 70
Db 226 GAGGAGTGTGATGGCTTGGAGCTGGTGAGAGTTCTCAGAGGACATGGAGAACATGCTG 285
Qy 71 ArgArgLysValGluAlaValGlnAenLeuValGluAlaAlaGluGluAlaAspLeuAen 90
Db 286 CGGAGGAAGTCGAGGCGGTCAGAAATCTGGTGAAGCTGCCGAGGAGCGGACCTGAAC 345
Qy 91 HisGluPheAenGlnSerLeuValPheAspTyrTyrAenSerValLeuIleAenGluArg 110
Db 346 CAGGAATTCGAATCCCTGGTGTTCGACTATTACAACTCGGTCTGTGATCAACGAGAGG 405
Qy 111 AspGluLysGlyAenPheValGluLeuGlyAlaGluPheLeuLeuGluSerAenAlaHis 130
Db 406 GACGAGAAGGGCAACTTCGTGGAGCTGGGCGCGAGTTCTCTCTGGAGTCCATGTCTAC 465
Qy 131 PheSerAenLeuProValAenThrSerIleSerSerValGlnLeuProThrAenValTyr 150
Db 466 TTCAGCAACCTGCGCGGTGAACACCTCCATCAGCAGCGTGCGACCTGCCCAACAGTGTAC 525
Qy 151 AsnLysAspProAspIleLeuAenGlyValTyrMetSerGluAlaLeuAenAlaValPhe 170
Db 526 AACAAAGACCCAGATATTTTAAATGGAGTGTACATGTCCTGAAGCCTTGAATGTGCTTC 585
Qy 171 ValGluAenPheGlnArgAspProThrLeuThrTyrPheGlySerAlaThrGly 190
Db 586 GTGGAGAACTTCCAGAGAGACCCACGTTGACCTGGCAATATTTTGGCAGTGCACCTGGA 645
Qy 191 PhePheArgIleTyrProGlyIleLysTyrThrProAspGluAenGlyValIleThrPhe 210
Db 646 TTCTTCAGGATCTATCCAGGTATAAAATGGACACCTGATGAGAATGGAGTCAATTACTTTT 705
Qy 211 AspCysArgAsnArgGlyTyrTyrIleGlnAlaAlaThrSerProLysAspIleValIle 230
Db 706 GACTGCGCAACCCGCGCTGTATCAATTCAGAGCTGTACTTCTCCCAAGGACATAGTGATT 765
Qy 231 LeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIle 250
Db 766 TTGGTGGACCTGAGCGGCAGTATGAAGGGCTGAGGATGACTATTGCCAAGCACACCATC 825
Qy 251 ThrThrIleLeuAspThrLeuGlyGluAenAspPheValAenIleIleAlaTyrAenAsp 270
Db 826 ACCACCATCTTGGACACCCCTGGGGGAGAATGACTTCGTTAATATCATAGCGTACAATGAC 885
Qy 271 TyrValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAen 290
Db 886 TAGCTCCATTACATCGAGCCTTGTTTTAAAGGATCTCTGTCAGCGGACCGAGACAAT 945
Qy 291 ArgGluHisPheLysLeuLeuValGluLeuMetValLysGlyValGlyValValAsp 310
Db 946 CGAGAGCATTTCAAACCTGCTGTGGAGAGTTGATGGTCAAAGGTGTGGGGTCTGGAC 1005
Qy 311 GlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySer 330
Db 1006 CAAGCCCTGAGAGAAGCCTTCCAGATCTCTAAGCAGTTCCAGAGGCCAAGCAAGGAAGC 1065
Qy 331 LeuCysAenGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProVal 350
Db 1066 CTCTGCACACCGGCCATCATGCTCATCAGCGCGCGCTGGAGGACTACGAGCCGGTG 1125
Qy 351 PheGluLysTyrAenTyrProAspCysLysValArgValPheThrTyrLeuIleGlyArg 370
Db 1126 TTTGAGAAGTATAACTGGCCAGACTGTAAAGTCCGAGTTTCACTTACCTCATTTGGAGA 1185
Qy 371 GluValSerPheAlaAspArgMetLysTyrPheIleAlaCysAenAenLysGlyTyrTyrThr 390

Db 1186 GAAGTGTCTTTTGTGACCCGCAATGAAGTGGATTGCATGCAACAACAAGGCTACTACACG 1245
Qy 391 GlnIleSerThrLeuAlaAspThrGlnGluAenValMetGluTyrIleuHisValLeuSer 410
Db 1246 CAGATCTCAACGCTGGCGGACACCCAGGAGAACTGATGGAATACCTGCAGCTGCTCAGC 1305
Qy 411 ArgProMetValIleAenHisAspHisAspIleIleTyrThrGluAlaTyrMetAspSer 430
Db 1306 CGCCCATCATGTCATCAACGACGACACATCATCTTGGACAGAGCCCTCATGGACAGC 1365
Qy 431 LysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProVal 450
Db 1366 AAGCTCTCAGCTCGCAGGCTCAGAGCCTGACACTGTTCACCACTGTGGCATGCCAGTC 1425
Qy 451 PheSerLysLysAenGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp 470
Db 1426 TTCAGCAAGAAGAACAAACGCGATCCCATGGCATTTCTCTGGGTGTGGGTCTCAGAT 1485
Qy 471 ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLys 484
Db 1486 GTGGCCCTGAGAGAGCTGATGAAGCTGGCGCCCGGTACAAAGATGCCAGCACAAACAGC 1545
Qy 485 -----LeuGlyValHisGlyTyrAlaPheLe 493
Db 1546 AGGCCTAATGCGCCTCCACCCCTGGACTCTGGCAGCTTGGAGTGCACGGATACGCTTTCT 1605
Qy 493 uAenThrAenAenGlyTyrIleLeuSerHisProAspLeuArgProLeuTyrArgGluGly 513
Db 1606 GAACACCAACAATGGGTACATCTCTCCCATCCCGACCTCCGCGCCCTGTACAGAGAGGG 1665
Qy 513 YLysLysLeuLysProLysProAenTyrAenSerValAspLeuSerGluValGluTyrpGly 533
Db 1666 GAAGAACAATAAAACCAACCTAACTACAAACAGTGTGGATCTCTCCGAAGTGGAGTGGGA 1725
Qy 533 uAspGlnAlaGluSerLeuArgThrAlaMetIleAenArgGluThrGlyThrLeuSerMe 553
Db 1726 AGACCAAGGCTGAATCTCTGAGAACAGCCATGATCAATAGGAAACAGGTACTCTCTCGAT 1785
Qy 553 tAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAenAspTyrPh 573
Db 1786 GGATGTGAAGGTTCGATGGAAGGAAAGCGAGTTCTTTCTGACCAATGACTACTT 1845
Qy 573 ePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArgGlyHisGly 593
Db 1846 CTTTCAGGACATCAGCGACACCCCTTTCAGTTTGGGGTGGTGTCTCTCCGGGGCCACCG 1905
Qy 593 yGluTyrIleLeuLeuGlyAenThrSerValGluGluGlyLeuHisAspLeuLeuHisPr 613
Db 1906 AGAATACATCTTCTGGGGAACACGCTCTGTGAAAGAAGGCTGCAATGACTTGTTCACCC 1965
Qy 613 oAspLeuAlaLeuAlaGlyAspTyrPheTyrCysIleThrAspIleAspProAspHisAr 633
Db 1966 AGACCTGGCCCTTGGCGGCTGACTTGGATCTACTGCAATCAGAGATATTGACCAAGACCCG 2025
Qy 633 gLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspProAspLeuGly 653
Db 2026 GAAGCTCGCCAGCTAGAGCCATGATCGCTTCTCCACAGGAAGAGCCACAGACCTGGA 2085
Qy 653 uCysAspGluGluLeuValArgGluValLeuPheAspAlaValThrAlaProMetGly 673
Db 2086 GTG----- 2088
Qy 673 uAlaTyrTrpThrAlaLeuAlaLeuAenMetSerGluGluSerGluHisValValAspMe 693
Db 2089 -----GAGTCTGAACACGTGGTGGACAT 2111
Qy 693 tAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGlySerGluGly 713
Db 2112 GGCTTCTTGGGACCCCGGCTCGCTCTGAGAACAGCAGCTTGTTCGTGGGCTCCGAGAA 2171
Qy 713 sValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThrLeuAspAr 733
Db 2172 GGTCTCCGACAGGAAGTTCTCTGACACCTGAGACGAGGCGCGGTGTTTCACTTGGACCG 2231


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Qy 733 gPheProLeuThrTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheValPheAnLe 753
Db 2332 CTTCCCGCTGTGTACCGCCAGGCTCAGACATCTGTGTCGACGCTTGTCTTCAACCT 2291
Qy 753 uArgTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAlaSerThrAl 773
Db 2292 CCGCTGGGCGAAGAGGACAGAAAGTGGGGGTGAACCCATGTGTGTGACGCGCAAGCAGC 2351
Qy 773 aValAlaValThrValAlaPheLysArgThrAlaAlaAlaAlaGlyValGlnMetLy 793
Db 2352 TGTGGCGGTGACCTGGACAGAGACAGCCATTTGCTGCAGCCCGGGCGGTCCAAATGA 2411
Qy 793 sLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThrValAspGl 813
Db 2412 GCTGGAATCTCTCAGCGCAAAATTTCTGGGGCGCAACGCGGAGTGCACACTGTGGATGG 2471
Qy 813 yProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAspAnAnGl 833
Db 2472 GCCGTGCACACAGAGCTGCGAGGACAGTGTCTGGACTGCTTCGTCATCGACAAACACGG 2531
Qy 833 yPheIleLeuIleSerLysArgSerArgGluThrGlyValArgPheLeuGlyGluValAspGl 853
Db 2532 GTTCATCTGTATCTCCAGAGGTCCGAGAGACCGGAAGATTTCTGGGGAGGTGGATGG 2591
Qy 853 yAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMetTyrAspTy 873
Db 2592 TGTCTGTCTCACCAGCTGCTCAGCATGGGGGTGTTCCAGCCAGTGCATGTATGACTA 2651
Qy 873 rGlnAlaMetCysLysProSerSerHisHisSerAlaAlaGlnProLeuValSerPr 893
Db 2652 TCAGGCCATGTGCAAAACCTCGAGTCCACACACAGTGCAGCCAGCCCTCTGGTCAGCCC 2711
Qy 893 oIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValLeuPheLeuLe 913
Db 2712 AATTCTGCTCTTTCAGCGGCGACAGGTGCTGTCAGGAGCTGTGTCTGTTCTCTGCT 2771
Qy 913 uGluTrpSerValTrpGlySerTrpTyrAspArgGlyValaGluAlaLysSerValPheHi 933
Db 2772 GGAGTGGAGTGTCTGGGGCTCTCTGTACGACAGAGGGCGCGAGCCAAAGTGTCTTCCA 2831
Qy 933 sHisSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGluTyrProVa 953
Db 2832 TCACTCCCAAAACACAGAGACGAGGACCCGCTCGAGCCCTCGCAGACACGGAGTACCCCGT 2891
Qy 953 lPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGlyProCysGl 973
Db 2892 GTTCTGTGTACCGCGCCATCCGGAGGCCAACGGGATGTGTGAGTCCGGGCCCTGCCA 2951
Qy 973 nLysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuValThrAspPr 993
Db 2952 GAAGTATTTGTGTGCAGCAGATTTCCCAACAGATACTCTCTCTCTGTTGACAGACCC 3011
Qy 993 oThrCysAspCysSerIlePheProProValLeuGlnGluAlaThrGluValLysTyrAs 1013
Db 3012 CACCTGTGACTGTCAGCATCTTCCACACAGTGTCTCGAGGAGCGCAGAAAGTCAAAATATA 3071
Qy 1013 nAlaSerValLysCysAspArgMetArgSerGlnLysAlaLeuArgArgProAspSerCy 1033
Db 3072 TGCCTCTGTCAATGTACCGGATGCGCTCCAGAGCCCGCGCGGACGACGACTCTGTG 3131
Qy 1033 sHisAlaPheHisProGluValArgValGluAlaAspArgGlyTrpAlaGlyPheSerSe 1053
Db 3132 CCACGCTTCCATCCAGAGGAGATGCCAGGACTGCGCGCGCGCTCGGACACCTCAGC 3191
Qy 1053 rProAsnProLeuCysLeuGlyLeuCysProCysArgGlnGluHisIleGlyMetProMe 1073
Db 3192 CTCGCGCGCCCTACTCTGCT-GCCTGTGTGTGCTGCGGGCTACTCGGCCCAACTCCTGC 3250
Qy 1073 tAsnThrPro 1076
Db 3251 GGTGACACCA 3260
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RESULT 15
AAD22004
ID AAD22004 standard; cDNA; 4125 BP.
XX
AC AAD22004;
XX
DT 12-FEB-2002 (first entry)
XX
DE Human transporters and ion channels (TRICH)-12 cDNA.
XX
KW Human; transporter and ion channel; TRICH; akinesia; cystic fibrosis;
KW diabetes mellitus; Parkinson's disease; myasthenia gravis; dementia;
KW cardiac disorder; angina; hypertension; myocarditis; hyperglycaemia;
KW neurological disorder; Alzheimer's disease; cataract; infertility;
KW Wilson's disease; schizophrenia; Grave's disease; Addison's disease;
KW Huntington's disease; multiple sclerosis; meningitis; hypotensive;
KW cardiant; nootropic; neuroprotective; neuroleptic; ophthalmological;
KW antithyroid; anticonvulsant; goitre; antiinflammatory; ss.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT CDS 1..3933
FT /tag= a
FT /product= "Human transporters and ion channels (TRICH)-
FT 12"
XX
PN WO200177174-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-US011206.
XX
PR 06-APR-2000; 2000US-0195595P.
PR 12-APR-2000; 2000US-0196872P.
PR 20-APR-2000; 2000US-0199020P.
PR 28-APR-2000; 2000US-0200052P.
PR 05-MAY-2000; 2000US-0202348P.
PR 11-MAY-2000; 2000US-0203495P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Reddy R, Thornton M, Borowsky ML, Tang YT, Khan FA, Tribouley CM;
PI Gandhi AR, Yao MG, Sanjanwala MS, Baughn MR, Nguyen DB, Policky JL;
PI Yue H, Seilhauer JJ, Walla NK, Lal P, Kearney L, Walsh RT, Lu DAM;
PI Lu Y, Greene BD, Raumann BE, Patterson C;
XX
DR WPI; 2002-017448/02.
DR P-PSDB; AAE13285.
XX
PT Polypeptides of human transporters and ion channels, useful for
PT diagnosing, treating or preventing disorders of transport, neurological,
PT muscle, immunological and cell proliferative disorders.
XX
PS Claim 5; Page 147-148; 150pp; English.
XX
CC The invention relates to human transporters and ion channels (TRICH) and
CC the polynucleotides encoding them. The composition comprising TRICH or
CC agonist of TRICH is useful for treating a disease or condition associated
CC with decreased expression of functional TRICH or condition associated
CC with overexpression of TRICH respectively. The composition comprising Ab
CC is useful for diagnosing a condition of disease associated with
CC expression of TRICH in a subject, where the disorders include a transport
CC disorder such as akinesia, cystic fibrosis, diabetes mellitus,
CC Parkinson's disease, myasthenia gravis, cardiac disorders associated with
CC transport e.g. angina, hypertension, myocarditis, neurological disorders
CC associated with transport e.g. Alzheimer's disease, Wilson's disease,
CC schizophrenia, cataracts, infertility, hyperglycaemia, Grave's disease,
CC goitre, Addison's disease, Huntington's disease, dementia, multiple
CC sclerosis, bacterial and viral meningitis. TRICH DNA is useful for
CC generating a transcript image of a tissue or cell type, which represents
CC the global pattern of gene expression by a particular tissue or cell type
CC and for analysing the proteome of a tissue or cell type. TRICH DNA is
```


CC used in gene therapy. The present sequence is human TRICH12 cDNA

XX Sequence 4125 BP; 989 A; 1109 C; 1188 G; 839 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 4125
Score: 3808.00 Matches: 750
Percent Similarity: 80.90% Conservative: 4
Best Local Similarity: 80.47% Mismatches: 14
Query Match: 66.50% Indels: 164
DB: 6 Gaps: 2

US-09-833-222A-10 (1-1090) x AAD22004 (1-4125)

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QY 11 AspArgValLysLeuTTPAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLys 30
DB :::|
1120 GAAACAGTGAAGCTATGGGTGACACCTTCGGGGGACCTGTATAACACTGTGACCAA 1179
QY 31 TyrSerGlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIle 50
DB |
1180 TACTCAGGCTCTCTTGTCTGCAGAGAGTACAAAGATGTGGAGTCCAGTCTGAAGATC 1239
QY 51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu 70
DB |
1240 GAGGAGGTGGATGGCTTGGAGCTGGTGAAGATTCTCAGAGGACATGGAGAACATGCTG 1299
QY 71 ArgArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsn 90
DB |
1300 CGGAGGAAAGTCGAGGCGGTCCAGAAATCTGGTGAAGCTCCGAGGAGCGCCACTGAAC 1359
QY 91 HisGluPheAsnGluSerLeuVal----- 98
DB |
1360 CACGAATTCATGATGATCCCTGGTGGAACTGGCGTGGGAGTTGGCGTGGGGATGTCGGTG 1419
QY 98 ----- 98
DB |
1420 ACGCAGTCCGGCGTGGGAGTTGGCGTGGGATGTCGTGACGAGTCCGCGTGGGAGTT 1479
QY 98 ----- 98
DB |
1480 GCGGTGGGAGTGTCCATAACGCTGTCCGGCGTGGGAGTTGGCGTGGGGATGTCGGTAGG 1539
QY 98 ----- 98
DB |
1540 CAGTCCGGCGTGGGAGTTGGCGTGGGAGTGTCCGTGACGAGTCCGGCGTGGGAGTTGGC 1599
QY 98 ----- 98
DB |
1600 GTGGGATGTCCGTGACGAGTCCGGCGTGGGAGTTGGCGTGGGAGTGTCCGTGAGGCAG 1659
QY 98 ----- 98
DB |
1660 TCCGGCGTGGGAGTTGGCGTGGGAGTGTCCGTGACGAGTGTCCGTGGGGGTGTTCAGTGCC 1719
QY 98 ----- 98
DB |
1720 CAGCGCGCCCGGGGTGTTGTGTAGACTCTGTATGGCCGCCCGCGCCGCCCTCTCG 1779
QY 98 ----- 98
DB |
1780 TCCTCTCACCTGGCGCGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1839
QY 99 -----PheAspTyrTyrAsnSerValLeuIleAsnGlu 109
DB |
1840 TCCGTGGGCTTCAACCGTCCACCCAGTTTCGACTATTACAACTCGGTCCTGTATCAACGAG 1899
QY 110 ArgAspGluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAla 129
DB |
1900 AGGACGAGAGAGGCAACTCTTCGTGGAGCTGGCGCCCGAGTTCTCTCTCTGGAGTCCAATGCT 1959
QY 130 HisPheSerAsnLeuProValAsnThrSerIleSerValGlnLeuProThrAsnVal 149
DB |
1960 CACTTCAGCAACCTGCGGTTGAACACCTTCATCAGCAGCGTGCAGCTGCCACCAACGCTG 2019
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QY 150 TyrAsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaVal 169
DB |
2020 TACAACAAAGACCCAGATATTTTAAATGGAGTCTACATGTCTGAAGCCTTTGAATGCTGTC 2079
QY 170 PheValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThr 189
DB |
2080 TTCGTGGAGACTTCCAGAGAGACCCAACTTCACCTGGCAATATTTTGGCAGTGCACACT 2139
QY 190 GlyPhePheArgIleTyrProGlyIleLysTyrThrProAspGluAsnGlyValIleThr 209
DB |
2140 GGATTCTTCAGGATCTATCCAGGTATAAAATGGACACCTCATGAGAATGGAGTCATTACT 2199
QY 210 PheAspCysArgAsnArgGlyTyrTyrIleGlnAlaAlaThrSerProLysAspIleVal 229
DB |
2200 TTTGACTCGCGAAACCGCGCTGTATCACTCAAGCTGCTACTTCTCCCAAGGACATAGTG 2259
QY 230 IleLeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThr 249
DB |
2260 ATTTTGTGGACGTGAGCGGCAGTATGAAGGGCTGAGGATGACTATTGCCAAGCACACC 2319
QY 250 IleThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsn 269
DB |
2320 ATCACCACCATCTTGGACACCTTGGGGGAGAATGACTTCAATTAATATCATAGGCTACAAT 2379
QY 270 AspTyrValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAsp 289
DB |
2380 GACTAGTCCATTACATCAGCCCTTGTTTTAAAGGATCTCTCTCAGCGCGGACCGAGAC 2439
QY 290 AsnArgGluHisPheLysLeuLeuValGluLeuMetValLysGlyValGlyValVal 309
DB |
2440 AATCGAGAGCATTTTCAACTGTGTGTGGAGGAGTTGATGGTCAAGAGTGTGGGGTCTGTG 2499
QY 310 AspGlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGlnAlaLysGlnGly 329
DB |
2500 GACCAAGCCCTCGAGAGAGCTTCCAGATCCTCAAGCAGTTTCCAAGAGGCGCAAGCAAGGA 2559
QY 330 SerLeuCysAsnGlnAlaIleMetLeuIleSerAspGlyValaValGluAspTyrGluPro 349
DB |
2560 AGCCTCTGCAACCCAGCCCATCATGCTCATCAGCAGCGCGCGCTGGAGGACTACGAGCCG 2619
QY 350 ValPheGluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGly 369
DB |
2620 GTGTTTGAAGATATAACTGGCCAGACTGTAAAGTCCGAGTTTCACTTACCTCATTTGGG 2679
QY 370 ArgGluValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyr 389
DB |
2680 AGAGAAGTGTCTTTTCTGACCGCATGAAGTGGATTGCAATGCACCAACAAGAGCTACTAC 2739
QY 390 ThrGlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeu 409
DB |
2740 AGCAGATCTCAACGCTGGCGGACCCAGGAGAACGTATGGAATACCTGCACGTGCTC 2799
QY 410 SerArgProMetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAsp 429
DB |
2800 AGCGCGCCCATGTGTATCAACCCAGCACCATCATCTGGACAGAGGCTTACATGGAC 2859
QY 430 SerLysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetPro 449
DB |
2860 AGCAAGCTCTCTCAGCTCGCAGGCTCAGAGCCTGACACTGCTCACCCTGTGGCCATGCCA 2919
QY 450 ValPheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySer 469
DB |
2920 GTCTTCAGCAAGAGAACCAACCGCATCCCATGGCATTTCTCTCTGGTGTGGTGGGCTCA 2979
QY 470 AspValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGly 489
DB |
2980 GATGTGGCCTCGAGAGAGCTGATGAAGCTGGCGCCCGGTACAAAGCTTGGAGTGCACGGA 3039
QY 490 TyrAlaPheLeuAsnThrAsnGlyTyrIleLeuSerHisProAspLeuArgProLeu 509
DB |
3040 TAGCGCTTTTGAACACCAACCAATGGCTACATCTCTCTCCATCCCGACCTCCGGCCCCGTG 3099
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Qy 510 TyrArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGlu 529
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Qy 530 ValGluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGly 549
Db |||||
3160 GTGGAGTGGGAAGACCAGGCTGAATCTCTGAGAACAGCCATGATCAATAGGGAACAGGT 3219
Qy 550 ThrLeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThr 569
Db |||||
3220 ACTCTCTCGATGGATGTGAAGTTCCGATGATAAAGGAAGCGAGTCTTTTCTCTGACC 3279
Qy 570 AsnAspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSer 589
Db |||||
3280 AATGACTACTTCTTCCAGGACATCAGCGACACCCCTTTTCAGTTTGGGGGTGGTGTCTCC 3339
Qy 590 ArgGlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAsp 609
Db |||||
3340 CGGGGCCACGGAGAAATACATCTTCTGGGGAAACAGTCTGTGGAAGAGGCTGCATGAC 3399
Qy 610 LeuLeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAsp 629
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3400 TTGCTTCACCCAGACTTGGCCCTGGCCGTGACTGGATCTACTGCATCACAGATATTGAC 3459
Qy 630 ProAspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAsp 649
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3460 CCAGACCACCGGAAGCTCAGCAGCTAGAGGCCATGATCCGCTTCTCACCCAGGAAGGAC 3519
Qy 650 ProAspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAlaValValThr 669
Db |||||
3520 CCAGACCTGGAGTGTGACGAGGAGCTGTCGGGAGGTGCTTGTGACCGGTGGTGACA 3579
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3580 GCCCCCATGGAAGCTACTGGACACGCTGGCCCTCAACATGTCGAGAGGTCTGAACAC 3639
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Db |||||
3700 GGCTCCGAGAAGGTCTCCGACAGGAAGTTCCTGACACCTGAGGACAGGCCAGCGTGTTC 3759
Qy 730 ThrLeuAspArgPheProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPhe 749
Db |||||
3760 ACCCTGGACCGCTTCCCGCTGTGGTACCGCCAGGCTCTCAGAGCATCTCTGCTGGCAGCTTC 3819
Qy 750 ValPheAsnLeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThr 769
Db |||||
3820 GTCTTCAACCTCCGCTGGGCAGAGGACCA-----GGACGCCCTTCTGCCAAAGGC 3870
Qy 770 AlaSerThrAlaValAlaValThrValAspLysArg 781
Db |||||
3871 CTTCCACCACCACTTTGCCAAACCATCTCTAAGCGT 3906
```

Search completed: November 17, 2005, 00:11:21
Job time : 1525 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2005, 03:09:42 ; Search time 171 Seconds
(without alignments)
2465.315 Million cell updates/sec

Title: US-09-833-222a-10
Perfect score: 5726
Sequence: 1 MAVALGTRRRDRVKLWADTF.....MPMNTVPVLLGGNIRVYAL 1090

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5726	100.0	1090	6	ABP59509 Human vol
2	5726	100.0	1090	7	ADF71820 Human cal
3	5386.5	94.1	1120	3	AAy92321 Human alp
4	5385.5	94.1	1207	7	ADe08021 Novel pro
5	5363	93.7	1097	4	AAu01038 Human sec
6	5363	93.7	1097	4	AB62262 Human cal
7	5276	92.1	1069	4	AAu01037 Human sec
8	5276	92.1	1069	4	AB62261 Human cal
9	5244.5	91.6	1096	3	AAy92324 Human alp
10	5234.5	91.4	1075	5	AAU09869 Novel hum
11	5230.5	91.3	1114	5	AAU09870 Novel hum
12	5179	90.4	1050	4	AAu01036 Human sec
13	5179	90.4	1050	4	AB62260 Human cal
14	4649	81.2	1096	3	AAy92323 Human alp
15	3808	66.5	1310	5	AAE13285 Human tra
16	3422	59.8	1091	5	AAE16666 Mouse cal
17	3419.5	59.7	1077	4	AAU01026 Human cal
18	3419.5	59.7	1077	4	AB62250 Human cal
19	3416.5	59.7	1091	5	AAE16665 Human cal
20	3410.5	59.6	1065	4	AAU01019 Human sec
21	3410.5	59.6	1085	3	AAy92320 Human alp
22	3410.5	59.6	1085	4	AAU01024 Human sec
23	3410.5	59.6	1085	4	AB62248 Human cal
24	3400.5	59.4	1071	4	AB62243 Human cal
25	3326.5	58.1	1038	4	AAU01018 Human sec

26	3326.5	58.1	1038	4	AB62242	Human cal
27	3278.5	57.3	1019	4	AAU01017	Human sec
28	3278.5	57.3	1019	4	AB62241	Human cal
29	3029.5	52.9	947	6	AB99658	Amino aci
30	2449	42.8	562	8	ADN33132	Human tra
31	2306	40.3	497	7	ADK40916	Novel hum
32	2306	40.3	497	8	ADR15609	Kinase 41
33	1870.5	32.7	519	3	AAy70460	Human mem
34	1792.5	31.3	350	4	AAU01022	Human sec
35	1792.5	31.3	350	4	AB62246	Human cal
36	1695	29.6	323	4	AAU01021	Human sec
37	1695	29.6	323	4	AB62245	Human cal
38	1598	27.9	304	4	AAU01020	Human sec
39	1598	27.9	304	4	AB62244	Human cal
40	1565	27.3	1258	8	ADO16905	Tobacco b
41	1554.5	27.1	1271	8	ADO16903	Tobacco b
42	1497.5	26.2	1215	4	AAE02340	D. melano
43	1410	24.6	2172	4	AB67958	Drosophil
44	1392.5	24.3	1245	8	ADO16901	Tobacco b
45	1322.5	23.1	1022	4	AB62234	Drosophil

ALIGNMENTS

RESULT 1
ABP59509
ID ABP59509 standard; protein; 1090 AA.
XX
AC ABP59509;
XX
DT 03-MAR-2003 (first entry)
XX
DE Human voltage gated calcium channel alpha2delta-4 subunit.

XX Human; voltage gated calcium channel; alpha2delta-4 subunit;
KW antiparkinsonian; tranquilizer; neuroprotective; anticonvulsant;
KW antimigraine; analgesic; cyostatic; antidepressant; antiinflammatory;
KW gene therapy; epilepsy; migraine; ataxia; vestibular defect;
KW chronic pain; neuropathic pain; Parkinson's disease; depression; cancer;
KW inflammation; seizure-related syndrome; anxiety; multiple sclerosis.
XX Homo sapiens.
OS
XX WO200283947-A2.
PN
XX 24-OCT-2002.
PD
XX 10-APR-2002; 2002WO-US011297.
PF
XX 11-APR-2001; 2001US-00833222.
PR
XX (ORTH) ORTHO-MCNEIL PHARM INC.
PA
XX Qin N, Codd E;
PI
XX WPI; 2003-093006/08.
DR
XX N-PSDB; ABZ20598.
DR
XX New nucleic acid molecule encoding human alpha2 delta4 calcium channel
PT subunit protein, useful for diagnosing and treating a disease associated
PT with defects in the subunit protein, e.g. epilepsy, migraine, ataxia or
PT chronic pain.
XX
PS Claim 13; Page 56-59; 91pp; English.
XX
CC The present invention provides the protein and coding sequences of human
CC voltage gated calcium channel alpha2delta-4 subunit. The sequences are
CC useful for diagnosing and treating a disease or disorder associated with
CC a defective alpha2delta-4 subunit, such as seizure-related syndromes,
CC epilepsy, migraine, ataxia, vestibular defects, chronic pain, neuropathic
CC pain, mood, sleep interference, anxiety, ALS, multiple sclerosis, mania,
CC Parkinson's disease, substance abuse/addiction syndromes, depression,

CC	cancer, or inflammation. The present sequence is the protein of the
CC	invention
XX	
SQ	Sequence 1090 AA;
QY	Query Match 100.0%; Score 5726; DB 6; Length 1090;
DB	Best Local Similarity 100.0%; Pred. No. 0;
DB	Matches 1090; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MAVALGTRRRDRVKLWADTGGDLVNTVTKYSGSLLLOKKYKDVESLKIIEVDGLVLR 60
DB	1 MAVALGTRRRDRVKLWADTGGDLVNTVTKYSGSLLLOKKYKDVESLKIIEVDGLVLR 60
QY	61 KFSDEMNLRRKVEAQNLVEAAEADLHNEFVESLVFDYVNSVLINERDEKGNFVELG 120
DB	61 KFSDEMNLRRKVEAQNLVEAAEADLHNEFVESLVFDYVNSVLINERDEKGNFVELG 120
QY	121 AEFLESNAHFSNLPVNTSISSVOLPTNVYNKDPDILNGVYMSEALNAVVENFQRDPTL 180
DB	121 AEFLESNAHFSNLPVNTSISSVOLPTNVYNKDPDILNGVYMSEALNAVVENFQRDPTL 180
QY	181 TWQYFGSATGFFRIYPGIKWTPDENGVIITDCNRGHWYIOAATSPKDIVILVDVSGSMKG 240
DB	181 TWQYFGSATGFFRIYPGIKWTPDENGVIITDCNRGHWYIOAATSPKDIVILVDVSGSMKG 240
QY	241 LRMTIAKHITITLTDLTGENDFVNI IAYNDYVHYIEPCFKGILVQADRDNRHFKLLVEE 300
DB	241 LRMTIAKHITITLTDLTGENDFVNI IAYNDYVHYIEPCFKGILVQADRDNRHFKLLVEE 300
QY	301 LMVKGVGVDQALREAFQILKQFEAKQGSCLCQAIMLISDGAVEDYEPVFEKYNPDCK 360
DB	301 LMVKGVGVDQALREAFQILKQFEAKQGSCLCQAIMLISDGAVEDYEPVFEKYNPDCK 360
QY	361 VRVFTYILIGREVSFADRMKIACNKGYYTQISTLADTQENVMYHLVSRPVMINHDD 420
DB	361 VRVFTYILIGREVSFADRMKIACNKGYYTQISTLADTQENVMYHLVSRPVMINHDD 420
QY	421 IIWTEAYMDSKLLSSQAQSITLTTVAMPVFSKNETRSHGILLGVGSDVALRELKMLA 480
DB	421 IIWTEAYMDSKLLSSQAQSITLTTVAMPVFSKNETRSHGILLGVGSDVALRELKMLA 480
QY	481 PRYKLGVGHVAFALNTNNGYITLHPDLRLPLRYREGKKLKPKNYNSVDLSEVWEQAE 540
DB	481 PRYKLGVGHVAFALNTNNGYITLHPDLRLPLRYREGKKLKPKNYNSVDLSEVWEQAE 540
QY	541 TAMINRETGLSDMKVPMQKGRVFLTNDYFTDIDTPFSLGAVLSRGHGEYILLGN 600
DB	541 TAMINRETGLSDMKVPMQKGRVFLTNDYFTDIDTPFSLGAVLSRGHGEYILLGN 600
QY	601 TSVEEGLHDLHPDLALAGDWIYICITDIDPHRKLQLEAMIRFLTRKDPDLSCDEELVR 660
DB	601 TSVEEGLHDLHPDLALAGDWIYICITDIDPHRKLQLEAMIRFLTRKDPDLSCDEELVR 660
QY	661 EVLFDVAVTAPMEAYWTALANMSESESHVVDMAFLGTRAGLRRSSLFVGSEKVSQRKFL 720
DB	661 EVLFDVAVTAPMEAYWTALANMSESESHVVDMAFLGTRAGLRRSSLFVGSEKVSQRKFL 720
QY	721 TPDEASVFTLDRPFLMYROASEHPAGSFVFNLRWAECPESAGEPMVVTASTAVATVDK 780
DB	721 TPDEASVFTLDRPFLMYROASEHPAGSFVFNLRWAECPESAGEPMVVTASTAVATVDK 780
QY	781 RTAIAAAGVQMKLEFLQRFKFAATROCSVTGDPYQTQSCDSLDLDCFVINDNNGFILLISK 840
DB	781 RTAIAAAGVQMKLEFLQRFKFAATROCSVTGDPYQTQSCDSLDLDCFVINDNNGFILLISK 840
QY	841 SRTGRFLGVDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHSAAQPLVSPISAF 900
DB	841 SRTGRFLGVDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHSAAQPLVSPISAF 900
QY	901 TRWLLQELVLFLEWSVWGSDYRGAEAKSVFHHSHKHKQDPLQCDTETYPVFNVPQAI 960
DB	901 TRWLLQELVLFLEWSVWGSDYRGAEAKSVFHHSHKHKQDPLQCDTETYPVFNVPQAI 960

QY	961 REANGIVEGCPCKQVFWQIQI PNSNLLLLVTDPTCDSCSIFPPVLQATEVKYNASVKCDR 1020
DB	961 REANGIVEGCPCKQVFWQIQI PNSNLLLLVTDPTCDSCSIFPPVLQATEVKYNASVKCDR 1020
QY	1021 MRSQKLRRRPDSCHAFHPEVRVEADRGWAGFSFSPNPLCLGLCPCRQEHIGMPNTPVPVL 1080
DB	1021 MRSQKLRRRPDSCHAFHPEVRVEADRGWAGFSFSPNPLCLGLCPCRQEHIGMPNTPVPVL 1080
QY	1081 LGGNIRVYAL 1090
DB	1081 LGGNIRVYAL 1090
RESULT 2	
ADP71820	
ID	ADP71820 standard; protein; 1090 AA.
XX	
AC	ADP71820;
XX	
DT	12-FEB-2004 (first entry)
DE	Human calcium channel alpha2delta4 subunit.
XX	
KW	neuroprotective; cytosolic; gene therapy; calcium channel;
KW	alpha2delta-4; amyotrophic lateral sclerosis; multiple sclerosis; cancer;
XX	human.
OS	Homo sapiens.
XX	
PN	US2003170785-A1.
XX	
PD	11-SEP-2003.
XX	
PF	10-APR-2002; 2002US-00119624.
XX	
PR	11-APR-2001; 2001US-00833222.
XX	
PA	{QINN/} QIN N.
PA	{CODD/} CODD E.
XX	
PI	Qin N, Codd E;
XX	
DR	WPI; 2003-898262/82.
DR	N-PSDB; ADP71819.
XX	
PT	New human alpha2 delta4 calcium channel subunit protein and nucleic acid
PT	molecule, useful for diagnosing and treating diseases associated with
PT	defective calcium channel subunit, e.g. cancer and multiple sclerosis.
XX	
PS	Claim 17; SEQ ID NO 10; 37pp; English.
XX	
CC	The invention describes a new isolated and purified nucleic acid molecule
CC	comprising: a sequence having at least a 70% identity to nucleotides 1-
CC	224 or 3308-3486 of a sequence of 3486 bp (S1) fully defined in the
CC	specification; at least 15 sequential bases of the polynucleotide of (a);
CC	or a sequence that is complementary to the polynucleotide of (a) or (b).
CC	Specifically claimed is an alpha2delta-4 nucleic acid molecule comprising
CC	a sequence of 3486 bp fully defined in the specification and encoding an
CC	alpha2delta-4 calcium channel subunit protein having a sequence of 1090
CC	amino acids fully defined in the specification. The nucleic acid molecule
CC	and polypeptide are useful in diagnosing and treating a disease or
CC	disorder associated with a defective alpha2delta-4 subunit, such as
CC	amyotrophic lateral sclerosis, multiple sclerosis or cancer. The methods
CC	may be used for identifying compounds capable of treating the above-
CC	mentioned diseases or disorders. This is the amino acid sequence of human
CC	calcium channel alpha2delta-4 subunit.
XX	
SQ	Sequence 1090 AA;

Query Match 100.0%; Score 5726; DB 7; Length 1090;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1090; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 1 MAVALGTRRRDRVKLWADTFGGDLYNTVTYKSGSLLLOKKYKDVESLSKIEEVDGLVLR 60
Db 1 MAVALGTRRRDRVKLWADTFGGDLYNTVTYKSGSLLLOKKYKDVESLSKIEEVDGLVLR 60

Qy 61 KPSEDMENLRRKVEAVQNLVEAAEADLNHERNESLVFDYNSVLINERDEKGNFVELG 120
Db 61 KPSEDMENLRRKVEAVQNLVEAAEADLNHERNESLVFDYNSVLINERDEKGNFVELG 120

Qy 121 AEFLLESNAHFSNLPVNTSISVQLPTNVYKOPDILNGVYMSALNAVFVENFQRPDPTL 180
Db 121 AEFLLESNAHFSNLPVNTSISVQLPTNVYKOPDILNGVYMSALNAVFVENFQRPDPTL 180

Qy 181 TWQYFGSATGFFRIYPGIKWTPDENGUITPDCNRGWIQAATSPKIDIVLVDVSGSMKG 240
Db 181 TWQYFGSATGFFRIYPGIKWTPDENGUITPDCNRGWIQAATSPKIDIVLVDVSGSMKG 240

Qy 241 LRMTIAKHITITLIDTIGENDFNIIAYNDVYHIEPCFKGILVQADRDRHFKLLAVEE 300
Db 241 LRMTIAKHITITLIDTIGENDFNIIAYNDVYHIEPCFKGILVQADRDRHFKLLAVEE 300

Qy 301 LMVKGVGVPDQALREAFQILKQFQAKGSLCNQAIMLISDGAVEDYEPVEKYNWPDCK 360
Db 301 LMVKGVGVPDQALREAFQILKQFQAKGSLCNQAIMLISDGAVEDYEPVEKYNWPDCK 360

Qy 361 VRVPTYLIGREVSADRMKWIACNNKGYITQISTLADTQENVMYHLVSRPMVINHDHD 420
Db 361 VRVPTYLIGREVSADRMKWIACNNKGYITQISTLADTQENVMYHLVSRPMVINHDHD 420

Qy 421 IITEAYWDSKLLSSQAQSLTLTTVAMPVFSKNETRSHGILLGVVGSVALRELKLA 480
Db 421 IITEAYWDSKLLSSQAQSLTLTTVAMPVFSKNETRSHGILLGVVGSVALRELKLA 480

Qy 481 PRYKLGVHGVAFLNTNNGYILSHPDRLPLRREGKLLKPKPNYSVDLSEWEWDAQESLR 540
Db 481 PRYKLGVHGVAFLNTNNGYILSHPDRLPLRREGKLLKPKPNYSVDLSEWEWDAQESLR 540

Qy 541 TAMINRETGILSMVDKVPKMGKRVLFITNDYFPTDISDTPFSLGAVLSRGHGYYILLGN 600
Db 541 TAMINRETGILSMVDKVPKMGKRVLFITNDYFPTDISDTPFSLGAVLSRGHGYYILLGN 600

Qy 601 TSVEEGLHDLHLLPDALAGDWIYICITDIDPHRKLQLEAMIRFLTRKDPDLECEBLVR 660
Db 601 TSVEEGLHDLHLLPDALAGDWIYICITDIDPHRKLQLEAMIRFLTRKDPDLECEBLVR 660

Qy 661 EVLFDVAVTAPMEAYWTALALNMSESEHVVDMAFGLTRAGLLRSSLFVSGSEKVS DRKFL 720
Db 661 EVLFDVAVTAPMEAYWTALALNMSESEHVVDMAFGLTRAGLLRSSLFVSGSEKVS DRKFL 720

Qy 721 TPDEASVFTLDRPPLMYROASEHPAGSFVFNLRWAGSPSAGBPMVVTASTAVAVTDK 780
Db 721 TPDEASVFTLDRPPLMYROASEHPAGSFVFNLRWAGSPSAGBPMVVTASTAVAVTDK 780

Qy 781 RTAIAAAGVQMKLEFLQRFMAATROCSTVDGPTYTQSCSDSDLDLCFVINDNGFILLISK 840
Db 781 RTAIAAAGVQMKLEFLQRFMAATROCSTVDGPTYTQSCSDSDLDLCFVINDNGFILLISK 840

Qy 841 SRETGRFLGVDGAVLTQLLSMGVFSQVTMYDYQAMCKPSHHSAQAQPLVSPISAFLLTA 900
Db 841 SRETGRFLGVDGAVLTQLLSMGVFSQVTMYDYQAMCKPSHHSAQAQPLVSPISAFLLTA 900

Qy 901 TRWLLQBLVLFLLEWSVWGSDRGAEAKSVFHHSHKHKKQDPLQPCDTEYFPVYQPAI 960
Db 901 TRWLLQBLVLFLLEWSVWGSDRGAEAKSVFHHSHKHKKQDPLQPCDTEYFPVYQPAI 960

Qy 961 REANGIVECGPCQKVFVVOQIPNSNLLLLVTDPTDCDSI PPPVLQAEATEVKYNASVKCDR 1020
Db 961 REANGIVECGPCQKVFVVOQIPNSNLLLLVTDPTDCDSI PPPVLQAEATEVKYNASVKCDR 1020

Qy 1021 MRSQKLRRRDPDSCHAFPEVRVEADRGWAGFSSPNPLCLGICPCROBIGHMPMNTPPVVL 1080
Db 1021 MRSQKLRRRDPDSCHAFPEVRVEADRGWAGFSSPNPLCLGICPCROBIGHMPMNTPPVVL 1080

Qy 1081 LGGNIRVYAL 1090
```

```
Db 1081 LGGNIRVYAL 1090
```

RESULT 3

AA92321 ID AAY92321 standard; protein; 1120 AA.

XX AA92321;

XX 10-AUG-2000 (first entry)

XX Human alpha-2-delta-D calcium channel subunit.

XX alpha-2-delta-D; calcium channel subunit; 3p21.1; gabapentin; cytostatic; anticonvulsant; antimigrane; antiparkinsonian; antidepressant.

XX Homo sapiens.

XX WO2000020450-A2.

XX 13-APR-2000.

XX 07-OCT-1999; 99WO-US023519.

XX 07-OCT-1998; 98US-0103322P.

XX 30-OCT-1998; 98US-0106473P.

XX 29-DEC-1998; 98US-0114088P.

XX (WARN) WARNER LAMBERT CO.

XX Johns MA, Moldover B, Offord JD;

XX WPI; 2000-303744/26.

XX N-PSDB; AAA09254.

XX New human nucleic acids encoding the alpha2delta-C and alpha2delta-D proteins, useful in the treatment of epilepsy, migraine, chronic pain, anxiety, multiple sclerosis or cancer.

XX Claim 8; Page 67; 88pp; English.

XX The alpha-2-delta-D gene encodes a calcium channel subunit polypeptide. The gene has been mapped to chromosome 12p13.1. This gene and the related alpha-2-delta-C and -B genes are useful for protecting mammalian cells from abnormal calcium flux by introducing expression vectors containing the respective gene into mammalian cells. The antisense genes are also useful for treating or preventing epilepsy. The alpha-delta-2-A protein is a high-affinity binding target of the anti-convulsant drug gabapentin. Therefore, alpha-delta-2 proteins may also be targeted to treat seizure-related syndromes, migraine, ataxia, vestibular defects, chronic pain, sleep interference, anxiety, amyotrophic lateral sclerosis (ALS), multiple sclerosis, mania, tremor, parkinsonism, substance abuse or addiction syndromes, mood, depression or cancer.

XX Sequence 1120 AA;

Query Match 94.1%; Score 5386.5; DB 3; Length 1120;

Best Local Similarity 98.0%; Pred. No. 0;

Matches 1033; Conservative 5; Mismatches 13; Indels 3; Gaps 2;

Qy 11 DRVKLWADTFGGDLYNTVTYKSGSLLLOKKYKDVESLSKIEEVDGLVLRKFSDEMML 70

Db 58 ETVKLWADTFGGDLYNTVTYKSGSLLLOKKYKDVESLSKIEEVDGLVLRKFSDEMML 117

Qy 71 RRKVEAVQNLVEAAEADLNHERNESLVFDYNSVLINERDEKGNFVELCAEFLLESNAH 130

Db 118 RRKVEAVQNLVEAAEADLNHERNESLVFDYNSVLINERDEKGNFVELCAEFLLESNAH 177

Qy 131 FSNLPVNTSISVQLPTNVYKOPDILNGVYMSALNAVFVENFQRPDPTLTWYFGSATG 190

Db 178 FSNLPVNTSISVQLPTNVYKOPDILNGVYMSALNAVFVENFQRPDPTLTWYFGSATG 237


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Db 505 EVSFADRMKWIACNNKGYITQISTLADTQENVMBYLHVLSRPMVINHDHDIITWEAYMDS 564
Qy 431 KLLSSQASQLTLLTTVAMPVFSKKNETSRSHGILLGVGSDVALRELKMLAPRYKLGVHG 490
Db 565 KLLSSQASQLTLLTTVAMPVFSKKNETSRSHGILLGVGSDVALRELKMLAPRYKLGVHG 624
Qy 491 AFLNTNNGYILSHDPDLAPLREGKLLPKPKPNYSVDLSEVEWDOAESLRTAMINRETGT 550
Db 625 AFLNTNNGYILSHDPDLAPLREGKLLPKPKPNYSVDLSEVEWDOAESLRTAMINRETGT 684
Qy 551 LSMQVKVPMQKGRVFLFTNDYFTDIDSDTSPFSLGAVLSRGHGVIYLLGNTSVBEGHLDL 610
Db 685 LSMQVKVPMQKGRVFLFTNDYFTDIDSDTSPFSLGVVLSRGHGVIYLLGNTSVBEGHLDL 744
Qy 611 LHPDLALAGDWIYICITDIDPDHRLKSQLEAMIRFLTRKDPDLECDDEELVRELVFADVTA 670
Db 745 LHPDLALAGDWIYICITDIDPDHRLKSQLEAMIRFLTRKDPDLECDDEELVRELVFADVTA 804
Qy 671 PMEAYWTALANMSESEHVVDMAPLGTAGLLRSSLFVGSEKVSDRKFLTPDEASVFT 730
Db 805 PMEAYWTALANMSESEHVVDMAPLGTAGLLRSSLFVGSEKVSDRKFLTPDEASVFT 864
Qy 731 LDRPPLVROASHPAGSFVFNLRWAGPESAGPMMVVTASTAVAVTVDKRTAIAAAGV 790
Db 865 LDRPPLVROASHPAGSFVFNLRWAGPESAGPMMVVTASTAVAVTVDKRTAIAAAGV 924
Qy 791 QMKLEFLQRKFWAATRCQSTVDGPTYQSCSDSDLDLDCFDVNDNGFILSKRSRETGRFLGE 850
Db 925 QMKLEFLQRKFWAATRCQSTVDGPTYQSCSDSDLDLDCFDVNDNGFILSKRSRETGRFLGE 984
Qy 851 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHSAAQPLVSPISAFLTATRWLLQBLVL 910
Db 985 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHSAAQPLVSPISAFLTATRWLLQBLVL 1044
Qy 911 FLEWSVWGSWYDRGAESKSVFHHSHKHKKQDPLQPCDTEPVPVYQPAIREANGIVECG 970
Db 1045 FLEWSVWGSWYDRGAESKSVFHHSHKHKKQDPLQPCDTEPVPVYQPAIREANGIVECG 1104
Qy 971 PCQKRVFVQQIPNSNLLLVTDPTCDGCSIFPPVLQEAATEVKYNASVKCDRMRSQKLRPP 1030
Db 1105 PCQKRVFVQQIPNSNLLLVTDPTCDGCSIFPPVLQEAATEVKYNASVKCDRMRSQKLRPP 1164
Qy 1031 DSCHAFHPEVRVADRQWAGFSSNP--LCIGLC 1062
Db 1165 DSCHAFHPEVNAQ--DCGASDTSAPPLLLPVC 1197

RESULT 5
AAU01038
XX AAU01038 standard; protein; 1097 AA.
AC AAU01038;
XX
DT 04-JUL-2001 (first entry)
XX
DE Human secreted soluble alpha2delta calcium channel subunit #18 protein.
XX
KW Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;
KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;
KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;
KW filter binding assay; wheat germ lectin flashplate assay.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 747..749 /note="Encoded by GCTGCG"
FT FT
FT Misc-difference 763..764 /note="Encoded by TCCGAGTGCCTCCTGAGAAGCAG
FT FT CTTGTCGTGCGCTCCGAGAAGGCTCCGAC"
XX
PN W0200119870-A2.
```

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XX 22-MAR-2001.
XX 18-SEP-2000; 2000WO-EP009137.
XX 16-SEP-1999; 99US-00397550.
XX (WARN ) WARNER LAMBERT CO.
XX Brown JP, Bertelli F;
XX WPI; 2001-235262/24.
XX N-PSDB; AAS01433.
XX Calcium channel alpha2delta subunits, useful in e.g. SPA assays,
XX Flashplate assays, Nickel Flashplate assays, Filter binding assays or
XX Wheat Germ Lectin Flashplate assays.
XX Claim 27; Page 156-160; 160pp; English.
XX The present sequence represents human secreted calcium channel
XX alpha2delta subunit #18 which is soluble and retains the functional
XX characteristics of the full length or wild type alpha2delta subunit
XX (AAU01025) from which it is derived. The invention relates to truncated
XX alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins
XX which retain their affinity for radioactively labelled gabapentin. The
XX alpha2delta subunit is 1 of the components of the heteromultimeric
XX voltage-dependent calcium channel (VDCC) complexes present in neuronal
XX and non-neuronal tissues including heart and skeletal muscle. Numerous
XX soluble forms of the human calcium channel alpha2delta subunits (AAU01014
XX -AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the porcine
XX calcium channel alpha2delta subunits (AAU01027-AAU01031) are described.
XX The secreted soluble alpha2delta subunit may be used in assays e.g.
XX scintillation proximity assay (SPA), flashplate, nickel flashplate,
XX filter binding or wheat germ lectin flashplate assays to detect or
XX measure the binding or interaction of a ligand (e.g. gabapentin, L-
XX Norleucine, L-Allo-Isoleucine, L-methionine, L-Leucine, L-Isoleucine, L-
XX Valine, Spermine and/or L-Phenylalanine) of a calcium channel alpha2delta
XX subunit
XX SQ Sequence 1097 AA;
XX
XX Query Match 93.7%; Score 5363; DB 4; Length 1097;
XX Best Local Similarity 98.8%; Pred. No. 0;
XX Matches 1028; Conservative 2; Mismatches 8; Indels 2; Gaps 2;
Qy 11 DRVKLWADTFGGDLVNTVTYKSGSLLLQKKYKQVSESSLKIEEVDGLSVRKFSDEMNL 70
Db 58 ETVKLWADTFGGDLVNTVTYKSGSLLLQKKYKQVSESSLKIEEVDGLSVRKFSDEMNL 117
Qy 71 RRKVEAVQNLVEAAEADLNHEFNESLVFDYNSVLINERDEKGNFVELGAEFLLESNAH 130
Db 118 RRKVEAVQNLVEAAEADLNHEFNESLVFDYNSVLINERDEKGNFVELGAEFLLESNAH 177
Qy 131 FSNLPVNTSISVOLPTNVNKKOPDILNGVYMSALNAVFNENFQDPTLTWQYFGSATG 190
Db 178 FSNLPVNTSISVOLPTNVNKKOPDILNGVYMSALNAVFNENFQDPTLTWQYFGSATG 237
Qy 191 FFRIYPGIKWTPDENGVIITFDCRNRGWYIOAATSPKDIIVLDVDSGSMKGLRMTIAKHTI 250
Db 238 FFRIYPGIKWTPDENGVIITFDCRNRGWYIOAATSPKDIIVLDVDSGSMKGLRMTIAKHTI 297
Qy 251 TTILDTLGENDFVNI IAYNDYVHYIEPCFPGILVQADRDNRHFKLLVEELMVGVGVD 310
Db 298 TTILDTLGENDFVNI IAYNDYVHYIEPCFPGILVQADRDNRHFKLLVEELMVGVGVD 357
Qy 311 QALREAFQILKQFOEAKQKSLCNOAIMLISDGAVEDYEPVEKYNWPCDKVRVFTYLIGR 370
Db 358 QALREAFQILKQFOEAKQKSLCNOAIMLISDGAVEDYEPVEKYNWPCDKVRVFTYLIGR 417
Qy 371 EVSFADRMKWIACNNKGYITQISTLADTQENVMBYLHVLSRPMVINHDHDIITWEAYMDS 430
Db 418 EVSFADRMKWIACNNKGYITQISTLADTQENVMBYLHVLSRPMVINHDHDIITWEAYMDS 477
```

QY 431 KLLSSQASQLTLTTVAMPVFSKQNETRSHGILLGVGVSDVALRELKMLAPRYKLGVHG 490
 Db 478 KLLSSQASQLTLTTVAMPVFSKQNETRSHGILLGVGVSDVALRELKMLAPRYKLGVHG 537
 QY 491 AFLNTNNGYILSHPDRLPLVREGKLLKPKPNYNSVDLSEVEWEDQABSLRTAMINRETGT 550
 Db 538 AFLNTNNGYILSHPDRLPLVREGKLLKPKPNYNSVDLSEVEWEDQABSLRTAMINRETGT 597
 QY 551 LSMGVKPMGKGVLFITNDYFPTDSDTPFSLGAVLSRGHGYILLGNSTSVEEGLHDL 610
 Db 598 LSMGVKPMGKGVLFITNDYFPTDSDTPFSLGAVLSRGHGYILLGNSTSVEEGLHDL 657
 QY 611 LHPDLALAGDWIYICITIDDPHRLKLSQLEAMIRLTKDPDLECEBELVREVLFDVAVTA 670
 Db 658 LHPDLALAGDWIYICITIDDPHRLKLSQLEAMIRLTKDPDLECEBELVREVLFDVAVTA 717
 QY 671 PMEAYWTALALNMSSESHVVDMAFLGTRA-GLLRSSLFVGSEKVSQRKFLTPDEASVF 729
 Db 718 PMEAYWTALALNMSSESHVVDMAFLGTRA-GLLRSSLFVGSEKVSQRKFLTPDEASVF 777
 QY 730 TLDREPLWYQASHPAGSFVNLRWAEGPSAGEPMAVVTASTAVAVTVDKRTAIAAAG 789
 Db 778 TLDREPLWYQASHPAGSFVNLRWAEGPSAGEPMAVVTASTAVAVTVDKRTAIAAAG 837
 QY 790 VQMKLEFLQKFWAATRCSTVDGPTQSCSDSLDCFVIDNNGFILLISKRSTGRFLG 849
 Db 838 VQMKLEFLQKFWAATRCSTVDGPTQSCSDSLDCFVIDNNGFILLISKRSTGRFLG 897
 QY 850 EVDGAVLTQLLSMGVFSQVTWYDYQAMCKPSSHHSSAAQPLVSPISAFLATRWLLQELV 909
 Db 898 EVDGAVLTQLLSMGVFSQVTWYDYQAMCKPSSHHSSAAQPLVSPISAFLATRWLLQELV 957
 QY 910 LFLLEWSVGSWYDRGAESVPHSHKHKQDPLOPCDTEYFVYVQPAIREANGIVEC 969
 Db 958 LFLLEWSVGSWYDRGAESVPHSHKHKQDPLOPCDTEYFVYVQPAIREANGIVEC 1017
 QY 970 GPCQKVFVVOQIIPNSNLLLVLTPTDCSIFPPVLQEADEVKNASVKCDRMSQKLRRR 1029
 Db 1018 GPCQKVFVVOQIIPNSNLLLVLTPTDCSIFPPVLQEADEVKNASVKCDRMSQKLRRR 1077
 QY 1030 PDSCHAFHPVRVEADRGWA 1049
 Db 1078 PDSCHAFHPREENAQ-DCGGA 1096

RESULT 6
 AAB62262
 ID AAB62262 standard; protein; 1097 AA.
 AC AAB62262;
 XX
 DT 11-JUN-2001 (first entry)
 XX
 DE Human calcium channel alpha2delta subunit.
 DE
 DE Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;
 KW nervous system disorder; pain; epilepsy; anxiety; human.
 KW
 XX Homo sapiens.
 OS
 XX
 XX WO200120336-A2.
 PN
 XX
 PD 22-MAR-2001.
 XX
 PF 18-SEP-2000; 2000WO-EP009136.
 XX
 PR 16-SEP-1999; 99US-00397549.
 XX
 XX (WARN) WARNER LAMBERT CO.
 PA
 XX Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;
 PI
 XX

DR WP1; 2001-257902/26.
 XX
 PT Competitive binding assay for screening ligands which bind a cerebral
 PT cortical voltage-dependent calcium channel alpha2delta-1 subunit, where
 PT the ligands identified are useful for treating disorders of the nervous
 XX system, including pain.
 PS Disclosure; Page 154-157; 158pp; English.
 XX
 CC The invention relates to a new method for screening ligands which bind a
 CC cerebral cortical voltage-dependent calcium channel alpha2delta subunit,
 CC preferably alpha2delta-1 subunit. The method comprises contacting a
 CC secreted soluble recombinant alpha2delta-1 subunit with a ligand of
 CC interest and a labelled compound which binds the subunit, followed by
 CC measuring the level of binding of the labelled compound to alpha2delta-1
 CC subunit. The method is useful for screening ligands, preferably
 CC biologically active products that modulate a nervous system function,
 CC which bind a cerebral cortical voltage-dependent calcium channel
 CC alpha2delta-1 subunit. The ligands identified by the method are useful
 CC for treating disorders of the nervous system, including pain, epilepsy
 CC and anxiety. The present sequence represents a human calcium channel
 CC alpha2delta subunit
 XX
 SQ Sequence 1097 AA;
 Query Match 93.7%; Score 5363; DB 4; Length 1097;
 Best Local Similarity 98.8%; Pred. No. 0;
 Matches 1028; Conservative 2; Mismatches 8; Indels 2; Gaps 2;
 QY 11 DRVKLWADTFGGDLVNTVTKYSGSLLOKQKXDVSSSLKIEEVDGLVLRKFSDEMML 70
 Db :
 58 ETVKLWADTFGGDLVNTVTKYSGSLLOKQKXDVSSSLKIEEVDGLVLRKFSDEMML 117
 QY 71 RRKVEAVQNLVAAEADLNHEFNESLVPDYNSVLINERDEKGNFVELGAEFLLESNAH 130
 Db 118 RRKVEAVQNLVAAEADLNHEFNESLVPDYNSVLINERDEKGNFVELGAEFLLESNAH 177
 QY 131 FSNLPNTSISVOLPTNVTYKNDPDLGVNYSALNAVFNFORDPDLTWQYFGSATG 190
 Db 178 FSNLPNTSISVOLPTNVTYKNDPDLGVNYSALNAVFNFORDPDLTWQYFGSATG 237
 QY 191 FFRYPGKWTDPDENGVIITFCRNRGWYIQAATS PKDIVILVDVSGSMKGLRMTIAKHTI 250
 Db 238 FFRYPGKWTDPDENGVIITFCRNRGWYIQAATS PKDIVILVDVSGSMKGLRMTIAKHTI 297
 QY 251 TTILDTLGENDFVNIAYNDYVHYIEPCPKGILVQADRONRHFHKLVBELVMVGVD 310
 Db 298 TTILDTLGENDFVNIAYNDYVHYIEPCPKGILVQADRONRHFHKLVBELVMVGVD 357
 QY 311 QALREAFQILKQFORAKOGSLCNQAIMLISDGAVEDYEPVFEKYNWPCCKVRVFTYLIGR 370
 Db 358 QALREAFQILKQFORAKOGSLCNQAIMLISDGAVEDYEPVFEKYNWPCCKVRVFTYLIGR 417
 QY 371 EYSFADRMKWIACNNKNGYVYTIQISTLADTQENYMEYLHLVSRPMVINHDDHDIITWEAYMDS 430
 Db 418 EYSFADRMKWIACNNKNGYVYTIQISTLADTQENYMEYLHLVSRPMVINHDDHDIITWEAYMDS 477
 QY 431 KLLSSQASQLTLTTVAMPVFSKQNETRSHGILLGVGVSDVALRELKMLAPRYKLGVHG 490
 Db 478 KLLSSQASQLTLTTVAMPVFSKQNETRSHGILLGVGVSDVALRELKMLAPRYKLGVHG 537
 QY 491 AFLNTNNGYILSHPDRLPLVREGKLLKPKPNYNSVDLSEVEWEDQABSLRTAMINRETGT 550
 Db 538 AFLNTNNGYILSHPDRLPLVREGKLLKPKPNYNSVDLSEVEWEDQABSLRTAMINRETGT 597
 QY 551 LSMGVKPMGKGVLFITNDYFPTDSDTPFSLGAVLSRGHGYILLGNSTSVEEGLHDL 610
 Db 598 LSMGVKPMGKGVLFITNDYFPTDSDTPFSLGAVLSRGHGYILLGNSTSVEEGLHDL 657
 QY 611 LHPDLALAGDWIYICITIDDPHRLKLSQLEAMIRLTKDPDLECEBELVREVLFDVAVTA 670
 Db 658 LHPDLALAGDWIYICITIDDPHRLKLSQLEAMIRLTKDPDLECEBELVREVLFDVAVTA 717

Qy 671 PMEAYWTALANMSESEHVVDMFLGTRA-GLLRSSLFVGSEKVSQDKFLTPDEASVF 729
 Dd 718 PMEAYWTALANMSESEHVVDMFLGTRA-GLLRSSLFVGSEKVSQDKFLTPDEASVF 777
 Qy 730 TLDREFFLWYQASHPAGSFVFNLRWAGSPESAGPEPMVVTASTAVAVTVDKRTAIAAAG 789
 Dd 778 TLDREFFLWYQASHPAGSFVFNLRWAGSPESAGPEPMVVTASTAVAVTVDKRTAIAAAG 837
 Qy 790 VQMKLEFLQKFWAATRCQSTVDGPTTQSCEDSDLDLCFVIDNNGFILLISKRSRETGRFLG 849
 Dd 838 VQMKLEFLQKFWAATRCQSTVDGPTTQSCEDSDLDLCFVIDNNGFILLISKRSRETGRFLG 897
 Qy 850 EVDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHSAAQPLVSPISAFLATRLLQELV 909
 Dd 898 EVDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHSAAQPLVSPISAFLATRLLQELV 957
 Qy 910 LFLLEWSVGSWYDRGAEAKSVFHHSHKHKQDPLOQCDTEYFVYVQPAIRREANGIVEC 969
 Dd 958 LFLLEWSVGSWYDRGAEAKSVFHHSHKHKQDPLOQCDTEYFVYVQPAIRREANGIVEC 1017
 Qy 970 GPCQKVFVQQIPNSNLLLVTDPTCDCSIFPPVLOBATEVKYNASVKCDRMSRQKLRRR 1029
 Dd 1018 GPCQKVFVQQIPNSNLLLVTDPTCDCSIFPPVLOBATEVKYNASVKCDRMSRQKLRRR 1077
 Qy 1030 PDSCHAFHPVEVRVADRGWA 1049
 Dd 1078 PDSCHAFHPENQAQ-DCGGA 1096

RESULT 7

AAU01037
 ID AAU01037 standard; protein; 1069 AA.

AC AAU01037;

DT 04-JUL-2001 (first entry)

XX Human secreted soluble alpha2delta calcium channel subunit #17 protein.

DE Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;
 KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;
 XW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;
 XX filter binding assay; wheat germ lectin flashplate assay.

XX Homo sapiens.

OS WO200119870-A2.

PN 22-MAR-2001.

XX 18-SEP-2000; 2000WO-EP009137.

XX 16-SEP-1999; 99US-00397550.

XX (WARN) WARNER LAMBERT CO.

XX Brown JP, Bertelli F;

XX WPI; 2001-235262/24.

DR N-PSDB; AAS01432.

XX Calcium channel alpha2delta subunits, useful in e.g. SPA assays,
 PT Flashplate assays, Nickel Flashplate assays, Filter binding assays or
 XX Wheat Germ Lectin Flashplate assays.

PS Claim 28; Page 153-156; 160pp; English.

XX The present sequence represents human secreted calcium channel
 CC alpha2delta subunit #17 which is soluble and retains the functional
 CC characteristics of the full length or wild type alpha2delta subunit
 CC (AAU01025) from which it is derived. The invention relates to truncated
 CC alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins
 CC which retain their affinity for radioactively labelled gabapentin. The

CC alpha2delta subunit is 1 of the components of the heteromultimeric
 CC voltage-dependent calcium channel (VDCC) complexes present in neuronal
 CC and non-neuronal tissues including heart and skeletal muscle. Numerous
 CC soluble forms of the human calcium channel alpha2delta subunits (AAU01014
 CC -AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the porcine
 CC calcium channel alpha2delta subunits (AAU01027-AAU01031) are described.
 CC The secreted soluble alpha2delta subunit may be used in assays e.g.
 CC scintillation proximity assay (SPA), flashplate, nickel flashplate,
 CC filter binding or wheat germ lectin flashplate assays to detect or
 CC measure the binding or interaction of a ligand (e.g. gabapentin, L-
 CC Norleucine, L-Allo-Isoleucine, L-methionine, L-Leucine, L-Isoleucine, L-
 CC Valine, Spermine and/or L-Phenylalanine) of a calcium channel alpha2delta
 CC subunit.

XX Sequence 1069 AA;

Query Match 92.1%; Score 5276; DB 4; Length 1069;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1008; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 11 DRVKLWADTFGGDLXNTVTYKSGSLLLQKKYKDVESLSKIEEVDGLBVRKFSDEMNM 70
 Dd :
 58 ETVKLWADTFGGDLXNTVTYKSGSLLLQKKYKDVESLSKIEEVDGLBVRKFSDEMNM 117
 Qy 71 RRKVEAVQNIVEAAEADLNHEFNESLVFDYNSVLINERDEKGNFVGLGAEFLLESNAH 130
 Dd :
 118 RRKVEAVQNIVEAAEADLNHEFNESLVFDYNSVLINERDEKGNFVGLGAEFLLESNAH 177
 Qy 131 FSNLPVNTSISVOLPTNVYKDPDILNGVYMGSEALNAVFNFORPDTLTWQYFGSATG 190
 Dd :
 178 FSNLPVNTSISVOLPTNVYKDPDILNGVYMGSEALNAVFNFORPDTLTWQYFGSATG 237
 Qy 191 FFRYPGKWTDPDENGVIPTDCRNRGWYIOAATSPKDIVILVDVSGSMKGLRMTIAKHTI 250
 Dd :
 238 FFRYPGKWTDPDENGVIPTDCRNRGWYIOAATSPKDIVILVDVSGSMKGLRMTIAKHTI 297
 Qy 251 TTILDTLGENDFVNIITAYNDYVHYIIEPCFKGILVQADRDNRHFFKLAVEELMKVGVGVD 310
 Dd :
 298 TTILDTLGENDFVNIITAYNDYVHYIIEPCFKGILVQADRDNRHFFKLAVEELMKVGVGVD 357
 Qy 311 QALREAFQILKQFOEAKQKQSLCNOAIMLISDGAVEDYEPVEFKYNWPDCKVRVFTYILGR 370
 Dd :
 358 QALREAFQILKQFOEAKQKQSLCNOAIMLISDGAVEDYEPVEFKYNWPDCKVRVFTYILGR 417
 Qy 371 EVSFADRMKWIACNNKGYTQISTLADTQBNVMYHLVLSRPMVINHDHDIITWEAYMDS 430
 Dd :
 418 EVSFADRMKWIACNNKGYTQISTLADTQBNVMYHLVLSRPMVINHDHDIITWEAYMDS 477
 Qy 431 KLLSSQAQSLTLTTVAMPVFSKKNETRSKILGCVGSDVALBELMKLAPRYKLGVHG 490
 Dd :
 478 KLLSSQAQSLTLTTVAMPVFSKKNETRSKILGCVGSDVALBELMKLAPRYKLGVHG 537
 Qy 491 AFLNTNNGYILSHPDRLPLVREGKCLKPKPNYNSVDLSEVEWEDQAESLTAMINRETGT 550
 Dd :
 538 AFLNTNNGYILSHPDRLPLVREGKCLKPKPNYNSVDLSEVEWEDQAESLTAMINRETGT 597
 Qy 551 LSMDVKVPMDKGRVLFNTNDYFPTDISDTPFSLGAVLSRGHGEYILLGNNTSVEEGLHDL 610
 Dd :
 598 LSMDVKVPMDKGRVLFNTNDYFPTDISDTPFSLGAVLSRGHGEYILLGNNTSVEEGLHDL 657
 Qy 611 LHPDLALAGDWIYICITDIDDPHRLKLSOLEAMIRFLTRKDPDLCEDESLVREVLFDVVTA 670
 Dd :
 658 LHPDLALAGDWIYICITDIDDPHRLKLSOLEAMIRFLTRKDPDLCEDESLVREVLFDVVTA 717
 Qy 671 PMEAYWTALANMSESEHVVDMFLGTRA-GLLRSSLFVGSEKVSQDKFLTPDEASVF 730
 Dd :
 718 PMEAYWTALANMSESEHVVDMFLGTRA-GLLRSSLFVGSEKVSQDKFLTPDEASVF 777
 Qy 731 LDRFPLWYQASHPAGSFVFNLRWAGSPESAGPEPMVVTASTAVAVTVDKRTAIAAAGV 790
 Dd :
 778 LDRFPLWYQASHPAGSFVFNLRWAGSPESAGPEPMVVTASTAVAVTVDKRTAIAAAGV 837
 Qy 791 QMKLEFLQKFWAATRCQSTVDGPTTQSCEDSDLDLCFVIDNNGFILLISKRSRETGRFLGE 850

Db 838 QMKLEFLQRFKFAATRCQSTVDGCTQSCDSLDLCFVDNNGFILISKRSRETGRFLGE 897
Qy 851 VDGAVLTQLLSMGVFSQVTWYDYQAMCKPSSHHSAAQPLVSPISAFELTATRWLLQELVL 910
Db 898 VDGAVLTQLLSMGVFSQVTWYDYQAMCKPSSHHSAAQPLVSPISAFELTATRWLLQELVL 957
Qy 911 FLEWSVMGWDYRGAEAKSVFHHSHKHKQDPLOPCDTBYPVYQPAIREANGIVECG 970
Db 958 FLEWSVMGWDYRGAEAKSVFHHSHKHKQDPLOPCDTBYPVYQPAIREANGIVECG 1017
Qy 971 PCQKVFVVOQIPNSNLLLVTDPTCDGSIFFPVVLQATEVKYNASVKCDRMR 1022
Db 1018 PCQKVFVVOQIPNSNLLLVTDPTCDGSIFFPVVLQATEVKYNASVKCDRMR 1069

RESULT 8
AAB62261
ID AAB62261 standard; protein; 1069 AA.
XX
AC AAB62261;
XX
DT 11-JUN-2001 (first entry)
XX
Human calcium channel alpha2delta subunit.
DE
XX Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;
KW nervous system disorder; pain; epilepsy; anxiety; human.
KW
XX Homo sapiens.
XX
XX WO200120336-A2.
XX
XX 22-MAR-2001.
XX
XX 18-SEP-2000; 2000WO-EP009136.
XX
XX 16-SEP-1999; 99US-00397549.
XX
XX (WARN) WARNER LAMBERT CO.
XX
XX Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;
PI
XX WPI; 2001-257902/26.
XX
XX N-PSDB; AAF57569.
XX
XX Competitive binding assay for screening ligands which bind a cerebral
PT cortical voltage-dependent calcium channel alpha2-delta-1 subunit, where
PT the ligands identified are useful for treating disorders of the nervous
PT system, including pain.
XX
XX Disclosure; Page 151-154; 158pp; English.
XX
XX The invention relates to a new method for screening ligands which bind a
CC cerebral cortical voltage-dependent calcium channel alpha2delta subunit,
CC preferably alpha2delta-1 subunit. The method comprises contacting a
CC secreted soluble recombinant alpha2delta-1 subunit with a ligand of
CC interest and a labelled compound which binds the subunit, followed by
CC measuring the level of binding of the labelled compound to alpha2delta-1
CC subunit. The method is useful for screening ligands, preferably
CC biologically active products that modulate a nervous system function,
CC which bind a cerebral cortical voltage-dependent calcium channel
CC alpha2delta-1 subunit. The ligands identified by the method are useful
CC for treating disorders of the nervous system, including pain, epilepsy
CC and anxiety. The present sequence represents a human calcium channel
CC alpha2delta subunit
XX
XX Sequence 1069 AA;

Query Match 92.1%; Score 5276; DB 4; Length 1069;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1008; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

RESULT 9
AAY92324
ID AAY92324 standard; protein; 1096 AA.
XX

Qy 11 DRVKLWADTFGGDLYNTVTYKSGSLLLOKQKYDVESLSKIEEVDGLVELKRFSEDMENML 70
Db :
58 ETVKLWADTFGGDLYNTVTYKSGSLLLOKQKYDVESLSKIEEVDGLVELKRFSEDMENML 117
Qy 71 RRKVEAVQNLVEAAEADLNHEFNESLVFDYDYNVSLINERDEKGNFVELGABFLLBESNAH 130
Db 118 RRKVEAVQNLVEAAEADLNHEFNESLVFDYDYNVSLINERDEKGNFVELGABFLLBESNAH 177
Qy 131 FSNLPVNTSISVOLPTNVNKPDPDILNGVYMSSEALNAVVENFORDPTLTWYFGSATG 190
Db 178 FSNLPVNTSISVOLPTNVNKPDPDILNGVYMSSEALNAVVENFORDPTLTWYFGSATG 237
Qy 191 FFRYFGIKWTPDENGVIITFDCNRGWYIOAAATSPKDIVILVDVSGMKGRLMTIAKHTI 250
Db 238 FFRYFGIKWTPDENGVIITFDCNRGWYIOAAATSPKDIVILVDVSGMKGRLMTIAKHTI 297
Qy 251 TTILDTLGENDFVNIITAYNDYVHYIEPCFKGILVQADRDNRHFKLLVBEELMKVGUGVD 310
Db 298 TTILDTLGENDFVNIITAYNDYVHYIEPCFKGILVQADRDNRHFKLLVBEELMKVGUGVD 357
Qy 311 QALREAFQILKQFEAKQKSLCNQATMLISDGAVEDYEPVEKYNMPCDKVRVFTYLIIGR 370
Db 358 QALREAFQILKQFEAKQKSLCNQATMLISDGAVEDYEPVEKYNMPCDKVRVFTYLIIGR 417
Qy 371 EVSFADRMKWIACNNKGYTQISTLADTQENVMYELHLSRPMVINHDHDIITTEAYMDS 430
Db 418 EVSFADRMKWIACNNKGYTQISTLADTQENVMYELHLSRPMVINHDHDIITTEAYMDS 477
Qy 431 KLLSSQAQSLTLTLTTVAMPVFSKNETRSHGILLGVGSDVALRELKMLAPRYKLGVHGY 490
Db 478 KLLSSQAQSLTLTLTTVAMPVFSKNETRSHGILLGVGSDVALRELKMLAPRYKLGVHGY 537
Qy 491 AFLNTNNGVILSHPDRLPLYREGKLLPKPNYSVDLSEVEWEDQAESLTAMINRETGT 550
Db 538 AFLNTNNGVILSHPDRLPLYREGKLLPKPNYSVDLSEVEWEDQAESLTAMINRETGT 597
Qy 551 LSMDVKVPMDKGRVILFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNSTVEEGLHDL 610
Db 598 LSMDVKVPMDKGRVILFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNSTVEEGLHDL 657
Qy 611 LHPDLALAGDWIYCIITDIDPDHRKLSQLEAMIRFLTRKOPDLCEDBELVREVLFDVAVTA 670
Db 658 LHPDLALAGDWIYCIITDIDPDHRKLSQLEAMIRFLTRKOPDLCEDBELVREVLFDVAVTA 717
Qy 671 PMEAYWTALALANMSESEHVDMAFLGTRAGLLRSSLFVSGSEKVSDBKFLTPDEASVFT 730
Db 718 PMEAYWTALALANMSESEHVDMAFLGTRAGLLRSSLFVSGSEKVSDBKFLTPDEASVFT 777
Qy 731 LDRFFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAGV 790
Db 778 LDRFFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAGV 837
Qy 791 QMKLEFLQRFKFAATRCQSTVDGCTQSCDSLDLCFVDNNGFILISKRSRETGRFLGE 850
Db 838 QMKLEFLQRFKFAATRCQSTVDGCTQSCDSLDLCFVDNNGFILISKRSRETGRFLGE 897
Qy 851 VDGAVLTQLLSMGVFSQVTWYDYQAMCKPSSHHSAAQPLVSPISAFELTATRWLLQELVL 910
Db 898 VDGAVLTQLLSMGVFSQVTWYDYQAMCKPSSHHSAAQPLVSPISAFELTATRWLLQELVL 957
Qy 911 FLEWSVMGWDYRGAEAKSVFHHSHKHKQDPLOPCDTBYPVYQPAIREANGIVECG 970
Db 958 FLEWSVMGWDYRGAEAKSVFHHSHKHKQDPLOPCDTBYPVYQPAIREANGIVECG 1017
Qy 971 PCQKVFVVOQIPNSNLLLVTDPTCDGSIFFPVVLQATEVKYNASVKCDRMR 1022
Db 1018 PCQKVFVVOQIPNSNLLLVTDPTCDGSIFFPVVLQATEVKYNASVKCDRMR 1069

AC AAY92324;
XX 10-AUG-2000 (first entry)
XX
XX Human alpha-2-delta-D polypeptide from splice variant 1.
XX
XX alpha-2-delta-D; calcium channel; 12p13.3; gabapentin; cytostatic;
XX anticonvulsant; antimigraine; antiparkinsonian; antidepressant;
XX splice variant.
XX
XX Homo sapiens.
XX
XX W0200020450-A2.
XX
XX 13-APR-2000.
XX
XX 07-OCT-1999; 99WO-US023519.
XX
XX 07-OCT-1998; 98US-0103322P.
XX 30-OCT-1998; 98US-0106473P.
XX 29-DEC-1998; 98US-0114088P.
XX
XX (WARN) WARNER LAMBERT CO.
XX
XX Johns MA, Moldover B, Offord JD;
XX
XX WPI; 2000-303744/26.
XX N-PSDB; AAA09729.
XX
XX New human nucleic acids encoding the alpha2delta-C and alpha2delta-D
XX proteins, useful in the treatment of epilepsy, migraine, chronic pain,
XX anxiety, multiple sclerosis or cancer.
XX
XX Example 3; Page 73; 88pp; English.
XX
XX This alpha-2-delta-D polypeptide is encoded by a splice variant that
XX contains a 72 bp deletion of an internal exon. However, this sequence
XX does not appear to have been reproduced in full in the specification (see
XX AAA09729). The gene encodes a calcium channel subunit polypeptide. The
XX gene has been mapped to chromosome 12p13.1. This gene and the related
XX alpha-2-delta-C and -B genes are useful for protecting mammalian cells
XX from abnormal calcium flux by introducing expression vectors containing
XX the respective gene into mammalian cells. The antisense genes are also
XX useful for treating or preventing epilepsy. The alpha-delta-2-A protein
XX is a high-affinity binding target of the anti-convulsant drug gabapentin.
XX Therefore, alpha-delta-2 proteins may also be targeted to treat seizure-
XX related syndromes, migraine, ataxia, vestibular defects, chronic pain,
XX sleep interference, anxiety, amyotrophic lateral sclerosis (ALS), multiple
XX sclerosis, mania, tremor, parkinsonism, substance abuse or addiction
XX syndromes, mood, depression or cancer
XX
XX Sequence 1096 AA;
Query Match 91.6%; Score 5244.5; DB 3; Length 1096;
Best Local Similarity 95.7%; Pred.No. 0;
Matches 1009; Conservative 5; Mismatches 13; Indels 27; Gaps 3;
QY 11 DRVKLWADTFGGDLYNTVTYKSGSLLLQKKYKDVESLKIIEVDGLVRFKFSDEMNL 70
DB :
DB 58 ETVKLWADTFGGDLYNTVTYKSGSLLLQKKYKDVESLKIIEVDGLVRFKFSDEMNL 117
QY 71 RRRKVEAVQNLVEAAEADLNHEFNESLVFDYNSVLINERDEKGNFVELGAEFLLESNAH 130
DB 118 RRRKVEAVQNLVEAAEADLNHEFNESLVFDYNSVLINERDEKGNFVELGAEFLLESNAH 177
QY 131 FSNLPVNTSSVQLPNTVYKDPDILGVYMSALNAVFNENFQDPDTLTWQYFGSATG 190
DB 178 FSNLPVNTSSVQLPNTVYKDPDILGVYMSALNAVFNENFQDPDTLTWQYFGSATG 237
QY 191 FFRYFGIKWTPDENGVIITDCRNRGWYIQAAATSPKDIVLVDSGSMKGLRMTIAKHTI 250
DB 238 FFRYFGIKWTPDENGVIITDCRNRGWYIQAAATSPKDIVLVDSGSMKGLRMTIAKHTI 297

QY 251 TTILDTLGENDFVNIITAYNDYVHYIIEPCFKGILVQADRDNRHFKLLVBEELMWKGVGVVD 310
DB 298 TTILDTLGENDFVNIITAYNDYVHYIIEPCFKGILVQADRDNRHFKLLVBEELMWKGVGVVD 357
QY 311 QALREAFQILKQFEAKQKQSLCNQAMLIISDGAVEDYEPVEFKYNWPDCKVRVFTYLIIGR 370
DB 358 QALREAFQILKQFEAKQKQSLCNQAMLIISDGAVEDYEPVEFKYNWPDCKVRVFTYLIIGR 417
QY 371 EVSFADRMKWIACNNKGYTQISTLADTQENVMYHLVLSRPMVINHDHDIITWEAYMDS 430
DB 418 EVSFADRMKWIACNNKGYTQISTLADTQENVMYHLVLSRPMVINHDHDIITWEAYMDS 477
QY 431 KLLSSQAQSLTLTTLTVAMPVFSKKNETRSRSHGILLGVVSDVALRELKMLAPRYKLGVHG 490
DB 478 KLLSSQAQSLTLTTLTVAMPVFSKKNETRSRSHGILLGVVSDVALRELKMLAPRYKLGVHG 537
QY 491 AFLNTNNGYILSHPDRLPLRYREGKCLKPKENYNNSVDLSEVEDQABSLRTAMINRETGT 550
DB 538 AFLNTNNGYILSHPDRLPLRYREGKCLKPKENYNNSVDLSEVEDQABSLRTAMINRETGT 585
QY 551 LSMKVPMQDKGRVILFLNDFYFTDIDTFFSLGAVLSRGHGEYILLGNSTVEEGLHDL 610
DB 586 -----KRVLFNTNDFYFTDIDTFFSLGAVLSRGHGEYILLGNSTVEEGLHDL 633
QY 611 LHEDLALAGDWIYCIITDIDPDHRLKSOLEAMIRFLTRKOPDLCEDELVREVLFDVVTA 670
DB 634 LHEDLALAGDWIYCIITDIDPDHRLKSOLEAMIRFLTRKOPDLCEDELVREVLFDVVTA 693
QY 671 PMEAYWTALALNMSSESEHVVDMFLGTRAGLRSLSLVGSEKVSORKFLTPEDEASVFT 730
DB 694 PMEAYWTALALNMSSESEHVVDMFLGTRAGLRSLSLVGSEKVSORKFLTPEDEASVFT 753
QY 731 LDRFPLWYRQASEHPAGSFVFNLRWAEGBESAGEPMVVTASTAVAVTVDKRTAIAAAGV 790
DB 754 LDRFPLWYRQASEHPAGSFVFNLRWAEGBESAGEPMVVTASTAVAVTVDKRTAIAAAGV 813
QY 791 QMKLEFLQRFKFWAATQCSVTGPGYTCQSCDSLDLDCFVINDNNGFILLISKESRETRFLGE 850
DB 814 QMKLEFLQRFKFWAATQCSVTGPGYTCQSCDSLDLDCFVINDNNGFILLISKESRETRFLGE 873
QY 851 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAPLVSPISAFLTATRWLLQELVL 910
DB 874 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAPLVSPISAFLTATRWLLQELVL 933
QY 911 FLEWSVWGSWYDRGAEAKSVFHHSHKHKQDPLQPCDTEYPVFPVQPAIREANGIVECG 970
DB 934 FLEWSVWGSWYDRGAEAKSVFHHSHKHKQDPLQPCDTEYPVFPVQPAIREANGIVECG 993
QY 971 PCQKVFVVOQIPNSNLLLVTDPTDCSIFPPVLOEATEVKYNASVKCDRMSQKLRPRP 1030
DB 994 PCQKVFVVOQIPNSNLLLVTDPTDCSIFPPVLOEATEVKYNASVKCDRMSQKLRPRP 1053
QY 1031 DSCHAFPHPEVRVEADRGWAGFGSSPNP--LCLGLC 1062
DB 1054 DSCHAFPHPEVRVEADRGWAGFGSSPNP--LCLGLC 1086
RESULT 10
AAU09869
ID AAU09869 standard; protein; 1075 AA.
XX AAU09869;
XX AC AAU09869;
XX XX
DT 25-FEB-2002 (first entry)
XX
DE Novel human secreted protein #10.
XX
KW Secreted protein; cytostatic; immunosuppressive; vulnery; vaccine;
KW antiinflammatory; neuroprotective; nephrotropic; cardiovascular; human;
KW cancer; autoimmune disease; wound healing disorder; infection;
KW haematopoietic disorder; inflammatory disorder; infertility;
KW neurological disease; psychiatric disease; cardiovascular disease;
KW respiratory disease; renal; gastrointestinal.

CC interest and a labelled compound which binds the subunit, followed by
CC measuring the level of binding of the labelled compound to alphadelta-1
CC subunit. The method is useful for screening ligands, preferably
CC biologically active products that modulate a nervous system function,
CC which bind a cerebral cortical voltage-dependent calcium channel
CC alphadelta-1 subunit. The ligands identified by the method are useful
CC for treating disorders of the nervous system, including pain, epilepsy
CC and anxiety. The present sequence represents a human calcium channel
CC alphadelta subunit
XX
SQ Sequence 1050 AA;

Query Match 30.4%; Score 5179; DB 4; Length 1050;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 989; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 11 DRVLMWADTGGDLNTVTYKYSGLLQKKYKDVESLKIIEVDGLVRFKSFEDMENML 70
DB :|||||
DB 58 ETVKLWADTGGDLNTVTYKYSGLLQKKYKDVESLKIIEVDGLVRFKSFEDMENML 117
QY 71 RRKVEAVQNIVEAAEADLNHEFNESLVFDYNSVLINERDEKGNFVELGAELLESNAH 130
DB |||||||
DB 118 RRKVEAVQNIVEAAEADLNHEFNESLVFDYNSVLINERDEKGNFVELGAELLESNAH 177
QY 131 FSNLPVNTSSVQLPNTVYKNDPDLINGVYMSALNAVFNENFORDPTLTWYFGSATG 190
DB |||||||
DB 178 FSNLPVNTSSVQLPNTVYKNDPDLINGVYMSALNAVFNENFORDPTLTWYFGSATG 237
QY 191 FFRIYPGIKWTPDENGVIITDCNRGWYIOAATSPKDIVILVDVSGMKGRLMTIAKHTI 250
DB |||||||
DB 238 FFRIYPGIKWTPDENGVIITDCNRGWYIOAATSPKDIVILVDVSGMKGRLMTIAKHTI 297
QY 251 TTILDTLGENDFVNIAYNDVHYIEPCFKGILLVQADRDNRHFKLLVEELVMYKGVGVD 310
DB |||||||
DB 298 TTILDTLGENDFVNIAYNDVHYIEPCFKGILLVQADRDNRHFKLLVEELVMYKGVGVD 357
QY 311 QALREAFQILKQOEAKQKGLCQAIIMLISDGAVEDYEPVEFKYNWPDCKRVFTYLIGR 370
DB |||||||
DB 358 QALREAFQILKQOEAKQKGLCQAIIMLISDGAVEDYEPVEFKYNWPDCKRVFTYLIGR 417
QY 371 EVSFADRMKWIACNNKGYTYQISTLADTQENVMYELHVLSPVMIHNDHDIITEAYMDS 430
DB |||||||
DB 418 EVSFADRMKWIACNNKGYTYQISTLADTQENVMYELHVLSPVMIHNDHDIITEAYMDS 477
QY 431 KLLSSQAQSLTLTTVAMPVFSKNETRSHRGILLGVVGSVDVALRELKMLAPRYKLGVHG 490
DB |||||||
DB 478 KLLSSQAQSLTLTTVAMPVFSKNETRSHRGILLGVVGSVDVALRELKMLAPRYKLGVHG 537
QY 491 AFLNTNNGYILSHPDRLPLRYREGKLLKPKPNYNSVDLSEVEWEDQAESLRTAINRETGT 550
DB |||||||
DB 538 AFLNTNNGYILSHPDRLPLRYREGKLLKPKPNYNSVDLSEVEWEDQAESLRTAINRETGT 597
QY 551 LSMDVKVPMDKGRVLFNTNDYFTDTSDFPSLGAVLRSRGHEYILLGNITSVEEGLHDL 610
DB |||||||
DB 598 LSMDVKVPMDKGRVLFNTNDYFTDTSDFPSLGAVLRSRGHEYILLGNITSVEEGLHDL 657
QY 611 LHDPDLALAGDWIYCIITDIDPDHRLKSLQEAIRFLTRKDPDLCEDEBELVREVLFDVAVTA 670
DB |||||||
DB 658 LHDPDLALAGDWIYCIITDIDPDHRLKSLQEAIRFLTRKDPDLCEDEBELVREVLFDVAVTA 717
QY 671 PMEAYWTALALNSESSEHVVWDAFLGTRAGLIRSLFVSEKVSQRKFLTPDEASVFT 730
DB |||||||
DB 718 PMEAYWTALALNSESSEHVVWDAFLGTRAGLIRSLFVSEKVSQRKFLTPDEASVFT 777
QY 731 LDRFPLMYROASEHPAGSFVFNLRWAEKGPSSAGEPMVVTASTAVATVDRKTAIAAAGV 790
DB |||||||
DB 778 LDRFPLMYROASEHPAGSFVFNLRWAEKGPSSAGEPMVVTASTAVATVDRKTAIAAAGV 837
QY 791 QMKLEFLQRKFWAATRCQSTVDGPYQTQSCSDSLDCFDVDDNNGFILLIKSRETGRFLGE 850
DB |||||||
DB 838 QMKLEFLQRKFWAATRCQSTVDGPYQTQSCSDSLDCFDVDDNNGFILLIKSRETGRFLGE 897
QY 851 VDGAVLTQLLSMGVFSQVMTYDYQAMCKPSSHHSAAQPLVSPISAFLTATRWLLQELVL 910

DB 898 VDGAVLTQLLSMGVFSQVMTYDYQAMCKPSSHHSAAQPLVSPISAFLTATRWLLQELVL 957
QY 911 FLLEWVWGSWYDRGAEAASVHFHSHKHKQDPLQPCDTEYFVVFVQPAIREANGIVECG 970
DB |||||||
DB 958 FLLEWVWGSWYDRGAEAASVHFHSHKHKQDPLQPCDTEYFVVFVQPAIREANGIVECG 1017
QY 971 PCKQFVWQIQPNNSNLLLVTDPTCDCSIFPPV 1003
DB |||||||
DB 1018 PCKQFVWQIQPNNSNLLLVTDPTCDCSIFPPV 1050

RESULT 14
AA923233
ID AAY92323 standard; protein; 1096 AA.
XX
AC AAY92323;
XX
DT 10-AUG-2000 (first entry)
XX
DE Human alpha-2-delta-D polypeptide from splice variant 1.
XX
DE alpha-2-delta-D; calcium channel; 12p13.3; gabapentin; cytostatic;
KW anticonvulsant; antimigrane; antiparkinsonian; antidepressant;
KW splice variant.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 310
FT /note= "encoded by RTT"
XX
PN WO200020450-A2.
XX
PD 13-APR-2000.
XX
PF 07-OCT-1999; 99WO-US023519.
XX
PR 07-OCT-1998; 98US-0103322P.
PR 30-OCT-1998; 98US-0106473P.
PR 29-DEC-1998; 98US-0114088P.
XX
PA (WARN) WARNER LAMBERT CO.
XX
PI Johns MA, Moldover B, Offord JD;
XX
XX WPI; 2000-303744/26.
DR N-PSDB; AAA09278.
XX
XX New human nucleic acids encoding the alpha2delta-C and alpha2delta-D
PT proteins, useful in the treatment of epilepsy, migraine, chronic pain,
PT anxiety, multiple sclerosis or cancer.
XX
PS Example 3; Page 84; 88pp; English.
XX
CC The alpha-2-delta-D gene encodes a calcium channel subunit polypeptide.
CC The gene has been mapped to chromosome 12p13.1. This gene and the related
CC alpha-2-delta-C and -B genes are useful for protecting mammalian cells
CC from abnormal calcium flux by introducing expression vectors containing
CC the respective gene into mammalian cells. The antisense genes are also
CC useful for treating or preventing epilepsy. The alpha-delta-2-A protein
CC is a high-affinity binding target of the anti-convulsant drug gabapentin.
CC Therefore, alpha-delta-2 proteins may also be targeted to treat seizure-
CC related syndromes, migraine, ataxia, vestibular defects, chronic pain,
CC sleep interference, anxiety, amyotrophic lateral sclerosis (ALS), multiple
CC sclerosis, mania, tremor, parkinsonism, substance abuse or addiction
CC syndromes, mood, depression or cancer
XX
SQ Sequence 1096 AA;

Query Match 81.2%; Score 4649; DB 3; Length 1096;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 895; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 11 DRVKLWADTFGGDLVNTVTYKSGSLLLQKKYKDVESLSKIEEVDGLVLRKFSDEMNM 70
Db : |||||
QY 58 ETVKLWADTFGGDLVNTVTYKSGSLLLQKKYKDVESLSKIEEVDGLVLRKFSDEMNM 117
Db : |||||
QY 71 RRVKVEAVQNLVEAAEADLNHEFNSLAVFDYNSVLINERDEKGNFVELGAELLESNAH 130
Db : |||||
QY 118 RRVKVEAVQNLVEAAEADLNHEFNSLAVFDYNSVLINERDEKGNFVELGAELLESNAH 177
QY 131 FSNLPVNTSSVQLPNNVYKDDPDLINGVYMEALNAVFEVFPQDPPTLTWQYFGSATG 190
Db : |||||
QY 178 FSNLPVNTSSVQLPNNVYKDDPDLINGVYMEALNAVFEVFPQDPPTLTWQYFGSATG 237
QY 191 FFRYIPGIKWTPBENGVIITFCNRRGWYIOAATSPKDIVILVDVSGSMKGLRMTIAKHTI 250
Db : |||||
QY 238 FFRYIPGIKWTPBENGVIITFCNRRGWYIOAATSPKDIVILVDVSGSMKGLRMTIAKHTI 297
QY 251 TTILDTLGENDFVNIITAYNDVHYIEPCFKGILLVQADRDNRHFKLLVEELMVKGVGVND 310
Db : |||||
QY 298 TTILDTLGENDFXNIIAYNDVHYIEPCFKGILLVQADRDNRHFKLLVEELMVKGVGVND 357
QY 311 QALREAFQILKQAEKQSGSLCQAINLISDGAVEDYEPVFEKYNPDPCKVRVFTYLIGR 370
Db : |||||
QY 358 QALREAFQILKQAEKQSGSLCQAINLISDGAVEDYEPVFEKYNPDPCKVRVFTYLIGR 417
QY 371 EVSFADRMKWIACNNKGYTQISTLADTQBNVMEYLHLVLSRPMVINHDHDIITEAYMDS 430
Db : |||||
QY 418 EVSFADRMKWIACNNKGYTQISTLADTQBNVMEYLHLVLSRPMVINHDHDIITEAYMDS 477
QY 431 KLLSSQAQSLTLTTVAMPVFSKKNETRSRSHGILLGVVSDVALRELMLAPRYKLGHVGY 490
Db : |||||
QY 478 KLLSSQAQSLTLTTVAMPVFSKKNETRSRSHGILLGVVSDVALRELMLAPRYKLGHVGY 537
QY 491 AFLNTNNGYILSHPDRLPLRYRECKLKPKNYNSVDLSEVEWEDQAESLRTAMINRETGT 550
Db : |||||
QY 538 AFLNTNNGYILSHPDRLPLRYRECKLKPKNYNSVDLSEVEWEDQAESLRTAMINRETGT 597
QY 551 LSNMVKVPMDKGRVFLTNDFYFTDIDTPFSLGAVLSRGHGEYILLGNNTSVEEGLHDL 610
Db : |||||
QY 598 LSNMVKVPMDKGRVFLTNDFYFTDIDTPFSLGAVLSRGHGEYILLGNNTSVEEGLHDL 657
QY 611 LHPDLALAGDWIYCIITDIDPDHRLKSOLEAMIRFLTRKOPDLCEDBELVREVLFDAAVTA 670
Db : |||||
QY 658 LHPDLALAGDWIYCIITDIDPDHRLKSOLEAMIRFLTRKOPDLCEDBELVREVLFDAAVTA 717
QY 671 PMEAYWTALALNWESESEHVVDMAFLGTRAGLRSLSLVGSEKVSQRKFLTPDEASVFT 730
Db : |||||
QY 718 PMEAYWTALALNWESESEHVVDMAFLGTRAGLRSLSLVGSEKVSQRKFLTPDEASVFT 777
QY 731 LDRFPLWYRQASHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAGV 790
Db : |||||
QY 778 LDRFPLWYRQASHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAGV 837
QY 791 QMKLEFLQRFKWAATRCQSTVDGPYTTQSCSDSLDCFDVDDNNGFILLIKSRRETGRFLGE 850
Db : |||||
QY 838 QMKLEFLQRFKWAATRCQSTVDGPYTTQSCSDSLDCFDVDDNNGFILLIKSRRETGRFLGE 897
QY 851 VDGAVLTQLLSMGVFSQVTMYDQAMKPSHHSSAAQPLVSPISAFLTATRWLLQELVL 910
Db : |||||
QY 898 VDGAVLTQLLSMGVFSQVTMYDQAMKPSHHSSAAQPLVSPISAFLTATRWLLQELVL 957

RESULT 15
AAE13285
ID AAE13285 standard; protein; 1310 AA.
XX AAE13285;
AC AAE13285;
XX AAE13285;
DT 12-FEB-2002 (first entry)
XX Human transporters and ion channels (TRICH)-12.
DE Human; transporter and ion channel; TrICH; akinesia; cystic fibrosis;
KW

diabetes mellitus; Parkinson's disease; myasthenia gravis; dementia;
cardiac disorder; angina; hypertension; myocarditis; hyperglycaemia;
neurological disorder; Alzheimer's disease; cataract; infertility;
Wilson's disease; schizophrenia; Grave's disease; Addison's disease;
Huntington's disease; multiple sclerosis; meningitis; hypotensive;
cardiac; nootropic; neuroprotective; neuroleptic; ophthalmological;
antithyroid; anticonvulsant; goitre; antiinflammatory.
Homo sapiens.
WO200177174-A2.
18-OCT-2001.
06-APR-2001; 2001WO-US011206.
06-APR-2000; 2000US-0195595P.
12-APR-2000; 2000US-0196872P.
20-APR-2000; 2000US-019020P.
28-APR-2000; 2000US-0200552P.
05-MAY-2000; 2000US-020348P.
11-MAY-2000; 2000US-0203495P.
(INCY-) INCYTE GENOMICS INC.
Reddy R, Thornton M, Borowsky ML, Tang YT, Khan FA, Tribouley CM;
Gandhi AR, Yao MC, Sanjanwala MS, Baughn MR, Nguyen DB, Policky JL;
Yue H, Sellhammer JJ, Wallia NK, Lal P, Kearney L, Walsh RT, Lu DM;
Lu Y, Greene BD, Raumann BE, Patterson C;
WPI; 2002-017448/02.
N-PSDB; AAD22004.
Polypeptides of human transporters and ion channels, useful for
diagnosing, treating or preventing disorders of transport, neurological,
muscle, immunological and cell proliferative disorders.
Claim 1; Page 132-135; 150pp; English.
The invention relates to human transporters and ion channels (TRICH) and
the polynucleotides encoding them. The composition comprising TRICH or
agonist of TRICH is useful for treating a disease or condition associated
with decreased expression of functional TRICH or condition associated
with overexpression of TRICH respectively. The composition comprising Ab
is useful for diagnosing a condition of disease associated with
expression of TRICH in a subject, where the disorders include a transport
disorder such as akinesia, cystic fibrosis, diabetes mellitus,
Parkinson's disease, myasthenia gravis, cardiac disorders associated with
transport e.g. angina, hypertension, myocarditis, neurological disorders
associated with transport e.g. Alzheimer's disease, Wilson's disease,
schizophrenia, cataracts, infertility, hyperglycaemia, Grave's disease,
goitre, Addison's disease, Huntington's disease, dementia, multiple
sclerosis, bacterial and viral meningitis. TRICH DNA is useful for
generating a transcript image of a tissue or cell type, which represents
the global pattern of gene expression by a particular tissue or cell type
and for analysing the proteome of a tissue or cell type. TRICH DNA is
used in gene therapy. The present amino acid sequence is human TRICH12
protein
Sequence 1310 AA;
Query Match 66.5%; Score 3808; DB 5; Length 1310;
Best Local Similarity 80.5%; Pred. No. 0;
Matches 750; Conservative 4; Mismatches 14; Indels 164; Gaps 2;
QY 11 DRVKLWADTFGGDLVNTVTYKSGSLLLQKKYKDVESLSKIEEVDGLVLRKFSDEMNM 70
Db : |||||
QY 374 ETVKLWADTFGGDLVNTVTYKSGSLLLQKKYKDVESLSKIEEVDGLVLRKFSDEMNM 433
QY 71 RRVKVEAVQNLVEAAEADLNHEFNSLV----- 98
Db 434 RRVKVEAVQNLVEAAEADLNHEFNSLV----- 98

Qy	99	-----	98
Db	494	GVGMSITLSGVGVGMSVRQSGVGVGMSVTSQSGVGVGMSVTQSGVGVGMSVRQ	553
Qy	99	-----	98
Db	554	SGVGVGMSVTQSGVGFSAQAAAGACVDSDRPAPALSSSHLRRFSSLSACPGARAA	613
Qy	99	-----FDYNSVLINERDEKGNFVLCAGAEFLLESNAHFSNLPVNTSISSVQLPTNV	149
Db	614	SVGLTRPPQFDYNSVLINERDEKGNFVLCAGAEFLLESNAHFSNLPVNTSISSVQLPTNV	673
Qy	150	YNKDPDILNGVYMSSEALNAVVENFQRPDPLTWQYFGSATGFPRIYPGIIKWTDPDENGVIIT	209
Db	674	YNKDPDILNGVYMSSEALNAVVENFQRPDPLTWQYFGSATGFPRIYPGIIKWTDPDENGVIIT	733
Qy	210	FDCNRGMYIQATSPKDIIVLDVSGSMGLRMTIAKHITTTITLDTLGENDFWIIAYN	269
Db	734	FDCNRGMYIQATSPKDIIVLDVSGSMGLRMTIAKHITTTITLDTLGENDFWIIAYN	793
Qy	270	DYVHYIEPCFKGILLVQADNRNREHFLLVEELMVKGVVVDQALREAFQILKQFQEAQOG	329
Db	794	DYVHYIEPCFKGILLVQADNRNREHFLLVEELMVKGVVVDQALREAFQILKQFQEAQOG	853
Qy	330	SLCNOAILMISDGAVEDYEPVEFKYNWPCDKVRVFTYILIGREVSFADRMKWIACNNKGY	389
Db	854	SLCNOAILMISDGAVEDYEPVEFKYNWPCDKVRVFTYILIGREVSFADRMKWIACNNKGY	913
Qy	390	TQISTLADTQENWMEYLHVLSPMPVINHDHDIITWEAYMDSKLLSSOQSLTLLTTVAMP	449
Db	914	TQISTLADTQENWMEYLHVLSPMPVINHDHDIITWEAYMDSKLLSSOQSLTLLTTVAMP	973
Qy	450	VFSKKNETRSHGILLGVVGSVALRELMLKAPRYKLGHVGYAFLNTNNGVILSHPDRLPL	509
Db	974	VFSKKNETRSHGILLGVVGSVALRELMLKAPRYKLGHVGYAFLNTNNGVILSHPDRLPL	1033
Qy	510	YREGKKLKPKNYNSVDLSEVEDQAEISLRTAMINRETGTLSMDVKVPMDKGRVULFLT	569
Db	1034	YREGKKLKPKNYNSVDLSEVEDQAEISLRTAMINRETGTLSMDVKVPMDKGRVULFLT	1093
Qy	570	NDYFFTDISTPFSLGAVLSRGHGEYILLGNTSVEEGLHDLHPDLALAGDWIYCIITDID	629
Db	1094	NDYFFTDISTPFSLGAVLSRGHGEYILLGNTSVEEGLHDLHPDLALAGDWIYCIITDID	1153
Qy	630	PDRHKLSQLAMIRFLTRKDPDLECDLREVLFDVAVTAPMEAYWTALANMSESEH	689
Db	1154	PDRHKLSQLAMIRFLTRKDPDLECDLREVLFDVAVTAPMEAYWTALANMSESEH	1213
Qy	690	VVDMAFLGTAGLLRSLFVGSEKVSQRKFLTPEDEASVFTLDRFPLWYQASEHPAGSF	749
Db	1214	VVDMAFLGTAGLLRSLFVGSEKVSQRKFLTPEDEASVFTLDRFPLWYQASEHPAGSF	1273
Qy	750	VFNLRWAEGPESAGEPMVTTASTAVAVTVDKR	781
Db	1274	VFNLRWAEGPESAGEPMVTTASTAVAVTVDKR	1302

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